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US-10-311-455-90/c
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7485, Ap
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 11, Appl
Sequence 19, Appl
Sequence 2344, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 90, Appl
Sequence 89, Appl
                                                                                             (without alignments)
2194.362 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                      1 ggaacctgggggtcaggccc......cccgccgcgattcagagagc 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                                                                                                                                            Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_MBW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NBW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_NBW_PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NBW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/US08_NBW_PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NBW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
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18: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10A_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10A_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10A_PUB.seq:*
                                                                               May 7, 2004, 14:31:30 ; Search time 208.502 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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5 US-10-222-577-11

6 US-10-222-578-11

7 US-10-183-181-649

6 US-10-189-563-190

6 US-10-108-260A-2344

7 US-10-143-002-3
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15 US-10-311-455-89
15 US-10-156-761-7485
15 US-10-156-761-1
15 US-10-156-761-1
8 15 US-10-156-761-1
9 US-09-925-297-188
9 US-09-790-045-11
                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                  2941586 seqs, 2264995651 residues
                                                                                                                              US-10-071-411A-1_COPY_950_1050
101
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                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 99%
Listing first 45 summaries
                                                        nucleic search, using sw model
                                                                                                                                                                             IDENTITY NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                              seq length: 0
seq length: 2000000000
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16
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Match Length DB
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13249 1
1989 1
9025608
1596 1
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Perfect score:
                                                        nucleic
                                                                                                                                                                                                                                                               Minimum DB
Maximum DB
                                                                                                                                                      Sequence:
                                                                                                                                                                                                                  Searched:
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                                                                                Run on:
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| 15 | 27.8 | 27.5 | 2483 | 15 | US-10-325-891-3 | Sequence 1766, Ap. 16 | 27.8 | 27.5 | 14918 | 9 | US-09-764-864-1766 | Sequence 1766, Ap. 18 | 27.6 | 27.5 | 14918 | 9 | US-09-764-864 | Sequence 1766, Ap. 27.6 | 27.7 | 27.4 | 27.1 | 366 | 15 | US-10-087-192-1411 | Sequence 1411, Ap. 27.6 | 27.4 | 27.1 | 366 | 15 | US-10-040-682-5868 | Sequence 5868, Ap. 27.2 | 27.4 | 27.1 | 366 | 16 | US-10-057-475B-5868 | Sequence 5868, Ap. 27.2 | 27.4 | 27.1 | 366 | 16 | US-10-057-475B-5868 | Sequence 5868, Ap. 27.2 | 27.2 | 26.9 | 326 | 10 | US-09-764-881-39 | Sequence 39, Appl. 24 | 27.2 | 26.9 | 326 | 10 | US-09-764-881-39 | Sequence 39, Appl. 24 | 27.2 | 26.9 | 326 | 10 | US-09-764-881-39 | Sequence 39, Appl. 24 | 27.2 | 26.9 | 326 | 10 | US-09-764-881-39 | Sequence 39, Appl. 25 | 27.2 | 26.9 | 326 | 15 | US-09-764-881-39 | Sequence 39, Appl. 27 | 27.2 | 26.9 | 326 | 15 | US-09-764-881-39 | Sequence 39, Appl. 27 | 27.2 | 26.9 | 44179 | 13 | US-09-764-881-39 | Sequence 5738, Appl. 27 | 26.9 | 669 | 15 | US-01-156-761-7385 | Sequence 5738, Appl. 27 | 26.9 | 669 | 15 | US-01-156-761-7385 | Sequence 5738, Appl. 27 | 26.7 | 620 | 13 | US-01-156-761-7385 | Sequence 5738, Appl. 27 | 26.7 | 620 | 13 | US-01-156-761-7385 | Sequence 5738, Appl. 27 | 26.7 | 26.7 | 26.9 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6 | 32.6
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RESULT 1

US-10-311-455-90/C

Sequence 90, Application US/10311455

Publication No. US20030143605A1

SEQUENCE 90, Application Wo. US20030143605A1

SEPTICANT: DEERLY WE CORK, Alexander

APPLICANT: DEERLY WEAR

TITLE OF INVENTION: OUTCAIN WEAR

PRIOR APPLICANTION NUMBER: D1001-00-12-16

PRIOR APPLICANTION WEAR

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8949160 GACCCCGGCGATCGTCCCCATGGGCGGCGGCCGGACCGGGCTCGCGCGACGCCCCCTT 8949219
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                                                                                                                                                         Gaps
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                                                                                                    0
                                                  Length 1989;
                                                                                                    Indels
                                               Score 28.8; DB 15;
Pred. No. 4.8;
0; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (4187715)
OTHER INFORMATION: a, t, c, g, other or unknown
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APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIRA, TADAXOSHI
APPLICANT: SHIRA, TADAXOSHI
APPLICANT: SHIRA, TADAXOSHI
APPLICANT: SHIRA, TADAXOSHI
APPLICANT: HATTORI MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-226
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-06-30
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 1
LENGTH: 9025608
                                                                                                                                                                                                                                                                                                                    504 CATCCCGTACGAGGCCCATGACCCGGGC 531
                                                                                                                                                                                                                                                                  62 CACACCCTTCCAGGCATTTGCCCGCCGC 89
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APPLICANT: ISHIKAMA, UNN
APPLICANT: HORIKAMA, HIROSH
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATROORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CACACCCTTCCAGGCATTTGCCCGCCGC
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Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/10156761
Publication No. US20030119018A1
                                               28.5%;
58.0%;
                                                                                                    51; Conservative
                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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US-10-156-761-7485
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                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 42.8%; Score 43.2; DB 15; Length 13249; Best Local Similarity 71.0%; Pred. No. 8.9e-05; Matches 71; Conservative 0; Mismatches 28; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-89
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9030 ACACCCTTCCAAACATTTACCCGCCGCGGATTCAAAAAC 8992
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APPLICANT: ISHIKAMA, JUN
APPLICANT: HARINAMA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIVKI
APPLICANT: SAKAKI, YOSHIVKI
APPLICANT: SAKAKI, WASAHIRA
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
SPRIOR FILING DATE: 2001-05-30
                                                                                                                       US-10-311-455-89

Sequence 89, Application US/10311455

Publication No. US20030143606A1

GENERAL INFORMATION:
APPLICANT: OLEK, Alexander

APPLICANT: OLEK, Alexander

TITLE OF INVENTION: Oytosine methylation
TITLE OF INVENTION: Oytosine methylation
FILE REFERENCE: 5013.1014

CURRENT APPLICATION NUMBER: US/10/311,455

CURRENT APPLICATION NUMBER: PCT/EPD1/07537

PRIOR FILING DATE: 2001-07-02

PRIOR FILING DATE: 2001-07-02

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: DE 10032529.7

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR SEQ ID NOS: 2424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: OMURA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (1)..(1989
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US-10-156-761-7485
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NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13249
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APPLICANT: Hasebe, Akira
APPLICANT: Tsuchiya, Kenichi
APPLICANT: Horita, Mitsuo
TITLE OF INVENTION: Insertion Sequence Element Derived From Ralstonia Solanacearum
FILE REFERENCE: NANP108US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96 CYCCARGIGCAGGCAGAGCCCCCRGAGMCRIGGCCAGCCCTTCCSGCAGCTCXGAAGCCA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    255 GECAGCATGCGCCAACCGCTGCCCGCTCGCACCAGATAGCGCAAGGCGTTGACCACCTCC 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 CCCCAGCGGCGCGCGCCCAGGAGCGCGCGAAACCTTCTCCACCCTTCCAGGCA
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                                  Sequence 188 Application US/09925297
; Sequence 188 Application US/09925297
; Patent No. US20020081659A1
; Patent No. US20020081659A1
; APPLICANT: ROSEATION:
; APPLICANT: ROSEATION:
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA105
; CURRENT APPLICATION NUMBER: US/09/925,297
; CURRENT FILING DATE: 2001-08-10
; PRIOR FILING DATE: 2001-08-08
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 928
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.1%; Score 28.4; DB 9;
53.7%; Pred. No. 7.3;
Live 6; Mismatches 32;
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CURRENT FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 11
LENGTH: 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc feature
LOCATION: (293)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (350)
; OTHER INFORMATION: n equals a,t,g, or
US-09-925-297-188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 crescanscocosassoras 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application US/09790045; Patent No. US20020052047A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Ralstonia solanacearum FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 27.9%;
Best Local Similarity 59.3%;
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) NAME/KEY: CDS
; LOCATION: (44)...(865)
US-09-790-045-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 44; Conserva
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US-09-790-045-11/c
                             US-09-925-297-188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1252 AcadedredeccadedececedareadaaAedredecedecadeadedecadecadecadecadecadeda 1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
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                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                             Length 1596;
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                                                                                                                                                                                                                                                                                                                                                                                                                               39;
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                                                                                                                                                                                                                                                                                                                                                                                Score 28.6; DE
Pred. No. 5.7;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 CACCCTTCCAGGCATTTGCCCGCCGCGATTC 94
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APPLICANI: IKEDA, HARUO
APPLICANI: ISHIKAWA, JUN
APPLICANI: HORIKAWA, JUN
APPLICANI: SHIBA, TADAYOSHI
APPLICANI: SHIBA, TADAYOSHI
APPLICANI: SAKAKI, YOSHIYUKI
APPLICANI: HATTORI, MASAHIRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
ITILE REFERRICE: 249-262
CURRENT FILING DATE: 2002-05-29
CURRENT FILING DATE: 2002-05-39
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-06-30
PRIOR PILING DATE: 2001-06-30
PRIOR PILING DATE: 2001-06-30
PRIOR PILING DATE: 2001-06-30
SROID NO 1
SEQ ID NOS: 15109
SEQ ID NO 1
LENGTH: 9025608
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: UP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SUG ID NO 4833
; LENGTH: 1596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                28.3%;
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Best Local Similarity 57.1%;
Matches 52; Conservative
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: LOCATION: (4187715)

: OTHER INFORMATION: a, t, c,

US-10-156-761-1
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Best Local Similarity 57.15
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; LOCATION: (1)..(1596)
US-10-156-761-4833
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TYPE: DNA
CORGANISM: Homo sapiens
US-09-833-381-649
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US-09-833-381-649
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Publication No. US20030027340A1

GENERAL INFORMATION:
APPLICANT: Hasebe, Akira
APPLICANT: Horita, Mitsuo
TITLE OF INVENTION: Insertion Sequence Element Derived From Ralstonia
TITLE OF INVENTION: Solanacearum
FILE REFERENCE: NAMP108US
CURRENT APPLICATION NUMBER: US/10/222,578
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US/09/790,045
PRIOR FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.0
SEQ ID NO 11
FILENTH: 884
                                                                                                                           Sequence 11. Application US/10222577

Sequence 11. Application No. US2003009026A1

Publication No. US2003009026A1

GENERAL INFORMATION:
APPLICANT: Hasebe, Akira
APPLICANT: Hasebe, Akira
TTILE OF INVENTION: Insertion Sequence Element Derived From Ralstonia
TITLE OF INVENTION: Insertion Sequence Element Derived From Ralstonia
TITLE OF INVENTION: Solanacearum
FILE REFERENCE: NANP108US
CURRENT FILING DATE: 2001-08-16
CURRENT FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
SEQ ID NO 11

LENGTH: 884
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ilarity 59.3%; Pred. No. 8;
Conservative 0; Mismatches 33;
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                                      195 chcháchcechcháchách 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Ralstonia solanacearum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Ralstonia solanacearum
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; LOCATION: (44)...(865)
US-10-222-578-11
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; LOCATION: (44)...(865)
US-10-222-577-11
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Best Local Similarity
Matches 48; Conserva
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US-10-222-578-11/c
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Sequence 190, Application US/10159563
; Sequence 190, Application US/10159563
; Publication No. 10220040009154A1
; GENERAL INFORMATION:
    APPLICANT: Khan, Javed
    APPLICANT: Ringner, Markus
    APPLICANT: Ringner, Markus
    APPLICANT: Melzer, Paul
    APPLICANT: Melzer, Paul
    APPLICANT: Melzer, Paul
    APPLICANT: Melzer, Paul
    APPLICANT: Melzer, SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
    TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS
    TITLE OF INVENTION: UNGNER: US/10/159,563
    CURRENT PILING DATE: 2002-012-09
    PRIOR APPLICATION NUMBER: US 10/133,937
    PRIOR APPLICATION NUMBER: US 10/133,937
    PRIOR PILING DATE: 2002-04-25
    NUMBER OF SEQ ID NOS: 444
    SOFTWARE: Patentin version 3.1
    SEQ ID NO 190

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                                        11 gercasgececasgesgasasgegececasgesgegegegegasascereceasascer 70
0; Gaps
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Pred. No. 11; 
0; Mismatches 37; Indels
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27.5%; Score 27.8; Di
Best Local Similarity 59.5%; Pred. No. 10;
Matches 47; Conservative 0; Mismatches
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                                                                                                                                         195 CTCAAGTCGCACTCCCGACGC 175
                                                                                              69 TTCCAGGCATTTGCCCGCCGC
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Best Local Similarity 57.5%;
Matches 50; Conservative
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Publication No. US20030092895A1
GENERAL INFORMATION:
APPLICANT: LI, ET AL.
TITLE OF INVENTION: Human Potassium Channel 1 and 2 Proteins NUMBER OF SEQUENCE: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLIAN,
STREET: 6 BECKER PARM ROAD
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                                                                                                                                                                                                                                 DB 14; Length 2483;
                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                           37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPL: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/325,891
FILING DATE: 23-Dec-2002
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-415
                                                                                                                                                                                                                                 ; Score 27.8; DB; Pred. No. 10; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/009,492
FILING DATE: CURKADOM:
APPLICATION NUMBER: 08/464,340
FILING DATE: June 5,1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 515 eccececadecrecrecececerates 541
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SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                               TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                         65 ACCCTTCCAGGCATTTGCCCGCCGCGA 91
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TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 2483 BASE PAIRS
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2483 BASE PAIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 201-994-1744
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1 Similarity 57.5%;
50; Conservative C
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ZIP: 07068
COMPUTER READABLE FORM:
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STATE: NEW JERSEY
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Best Local Similarity
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Best Local Similarity
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  117 GGCGCTCGGCGTGCTGCTGCCTCCTTCCCCGCGCACGATGCCGTGTCCACCGCT
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                                                                                                                                                                                                                                                   APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20040005560Alel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT APPLICATION DOS: 5458
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE: CARRILA, BYRNE, BAIN, GILFILLAN,
FRCCHI, STEWART & OLSTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/10143002
Publication No. US20020132775A1
GENERAL INPORMATION:
APPLICANT: LI, ET AL.
TITLE OF INVENTION: Potassium Channel Protein 1
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CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/102,493
FILING DATE: «Unknown»
APPLICATION NUMBER: US/08/468,533
FILING DATE: 6 JUNE 1995
APPLICATION NUMBER: PCT/US94/08449
FILING DATE: 28 JUL 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 325800-310
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 27.8; DB
Pred. No. 10;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/143,002
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                                                                                                                                                                                     ; Sequence 2344, Application US/10108260A; publication No. US20040005560A1; GENERAL INFORMATION:
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STREET: 6 BECKER FARM ROAD
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                                                                                   57 Greencherecter 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 27.5%;
Best Local Similarity 74.5%;
Matches 35; Conservative
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ZIP: 07068
COMPUTER READABLE FORM:
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Sequence 649, Appli Sequence 3, Appli Sequence 31, Appli Sequence 171, App Sequence 171, App Sequence 1524, App Sequence 15295, Appli Sequence 2, Appli Sequence 2, Appli
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13396, A
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Sequence 1
Sequence 1
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-222-577-11
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US-09-489-039A-811
US-09-252-991A-13564
US-09-252-991A-15544
US-09-252-991A-15544
US-09-252-991A-13956
US-09-252-991A-133664
US-09-252-991A-133664
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US-09-252-991A-133664
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US-09-252-991A-13369
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Maximum Match 99%
Listing first 45 summaries
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Perfect score:
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Maximum DB :
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US-09-790-045-11/c

| US-09-790-045-11/c
| US-09-790-045-11/c
| Sequence 11, Application US/09790045
| Patent No. 6492510
| GENERAL INFORMATION:
| APPLICANT: Hasebe, Akira
| APPLICANT: Hasebe, Akira
| APPLICANT: Horita, Mitsuo
| TITLE OF INVENTION: Insertion Sequence Element Derived From Ralstonia Solanacearum
| Patent No. 6492510
| FILE REPERENCE: NANPIORS:
| CURRENT APPLICATION NUMBER: US/09/790,045
| CURRENT FILING DATE: 2001-02-21
| NUMBER OF SEQ ID NOS: 14
| SOFTWARE: PatentIn version 3.0
| SEQ ID NO 11
| LINGTH: 884
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                                                                                    Sequence 1288, A Sequence 11208, A Sequence 11046, A Sequence 15756, A Sequence 10971, A Sequence 9056, Ap Sequence 10, Appl Sequence 10, Appl Sequence 1556, A Sequence 1556, A Sequence 1568, A Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli
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               Sequence 19, Appli
Sequence 2, Appli
Sequence 1, Appli
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                                        3 US-09-103-840A-2

US-09-103-840A-1

US-09-252-991A-11208

US-09-252-991A-11206

US-09-252-991A-15756

US-09-252-991A-10971

US-09-252-991A-10971

US-09-252-991A-9066

US-09-252-991A-9066

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US-09-252-991A-1568

US-09-222-991A-1568

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Pred. No. 7.2;
0; Mismatches
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Patent No. 6538125
GREERAL INFORMATION:
APPLICANT: Hasebe, Akira
APPLICANT: Hasebe, Akira
APPLICANT: Hasebe, Akira
APPLICANT: Horita, Mitsuo
APPLICANT: Horita, Mitsuo
APPLICANT: Horita, Mitsuo
APPLICANT: NEWNION: Sequence Eleme
TITLE OF INVENTION: Solanacearum
CURRENT APPLICATION NUMBER: US/10/222,577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  195 CTCAAGTCGCACTCCCGACGC 175
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les 48; Conservative
) NAME/KEY: CDS
; LOCATION: (44)...(865)
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US-10-222-577-11/c
  Query Match
Best Local S:
Matches 48
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NAME: FERRARO, GREGORY D. REGISTRATION NUMBER: 36,134
REFERRANCE, DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELECHONE: 201-994-1700
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2483 BASE PAIRS
                                                                                                                                                                                                                                                                          27.5%;
                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 57.5
Matches 50; Conservative
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STRANDEDNESS: SINGLE
                                                                                                                                                                                               TYPE: DNA ORGANISM: Homo sapiens
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STATE: NEW JERSEY
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Best Local Similarity
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CITY: ROSELAND
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                                                                                                                                                                                                                                     US-09-833-381-649
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US-08-464-340A-3
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Sequence 11, Application US/1022578

Patent No. 657007

GENERAL INFORMATION:
APPLICANT: Hasebe, Akira
APPLICANT: Hasebe, Akira
APPLICANT: Horita, Mitsuo
TITLE OF INVENTION: Insertion Sequence Element Derived From Ralstonia
PILE REPERENCE: NANP108US
TITLE OF INVENTION: Solanacearum
FILE REPERENCE: NANP108US
CURRENT APPLICATION NUMBER: US/10/222,578
CURRENT APPLICATION NUMBER: US/09/790,045
PRIOR PPLICATION NUMBER: US/09/790,045

PRIOR PILLING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 14

SOFTHARE: PATENTING PATE: 2001-02-21

NUMBER OF SEQ ID NOS: 14

SEQ ID NO 11

LENGTH: 884
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                                                                                                                                                                                                                                                                                 DB 4; Length 884;
                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                 27.9%; Score 28.2; 59.3%; Pred. No. 7.
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US/09/790,045
PRIOR FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 11
LENGTH: 884
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ORGANISM: Ralstonia solanacearum
                                                                                                                                         TYPE: DNA
ORGANISM: Ralstonia solanacearum
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APPLICANT: Robison, Keith E.
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; LOCATION: (44)...(865)
US-10-222-578-11
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; LOCATION: (44)...(865)
US-10-222-577-11
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Best Local Similarity
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US-09-833-381-649
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TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs FILE REFERENCE: 5800-119
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR PILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SOFTWARE: PastSEQ for Windows Version 3.0
LENGTH: 412
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Patent No. 5710019
GENERAL INFORMATION:
APPLICANT: LI, ET AL.
TITLE OF INVENTION: Human Potassium Channel 1 and 2 Proteins
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,340A
FILING DATE: Unne 5,1995
CLASSIFICATION: 435
PRIOR APPLICATION 435
PRIOR APPLICATION WHERE: PCT/US94/08449
FILING DATE: 28 JUL 1994
ATTORNEY/AGENT INFORMATION:
AMPLICATION TOTAL 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 CCAGGCATTTGCCCGCCGCGATTCAGA 97
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FILING DATE: 1997-06-06
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Best Local Similarity
TITLE OF INVENTION:
TITLE OF INVENTION:
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US-09-205-258-171/c
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              37; Indels
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GENERAL INFORMATION:
APPLICANT: LI, FT AL.
TITLE OF INVENTION: Potassium Channel Protein 1 and 2
NUMBER OF SEQUENCES: 4
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ADDRESSEE: CRRELLA, BXRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
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57.5%; Pred. No. 11;
cive 0; Mismatches
              0; Mismatches
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MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: 1BM PS.
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION NUMBER: PCT/US94/0844
PILLING DATE: SUBMITTED HEREWITH
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Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,1
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 2483 BASE PAIRS TYPE: NUCLEIC ACID STRANDEDNESS: SINGLE
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Matches 50; Conservative
                      50; Conservative
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STATE: NEW JERSEY
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TOPOLOGY: LINEAR
MOLECULE TYPE: CDN
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PCT-US94-08449A-3
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
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Pred. No. 14;
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APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZ007P1
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER FILING DATE: 1998-12-04
EARLIER FILING DATE: 1998-06-04
EARLIER FILING DATE: 1998-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                    FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
LENGTH: 1665
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R PAPPLICATION NUMBER: 60/048,884
R PILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,894
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,971
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,971
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APPLICATION NUMBER: 60/048,900
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APPLICATION NUMBER: 60/049,020
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APPLICATION UNDRER: 60/048,876
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,895
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FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,901
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APPLICATION NUMBER: 60/049,375
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APPLICATION NUMBER: 60/048,881
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Patent No. 6525174
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CRGANISM: Klebsiella pneumoniae
US-09-489-039A-831
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US-09-252-991A-15544/c

10S-09-252-991A-15544/c

Sequence 15544 Application US/0925291A

Patent No. 6551795

GREERAL INFORMATION:
APPLICATION:
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 15544

LENGTH: 1326
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Pred. No. 21;
0; Mismatches 44; Indels
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                         Sequence 2262, Application US/09621976
Facent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET: 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
; SEQ ID NO 2262
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58.0%; Pred. No. 23;
tive 0; Mismatches 34;
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ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity 54.6%;
Matches 53; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: 216..368
US-09-621-976-2262
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                   JS-09-621-976-2262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.7%; Score 27; DB 4; Length 2003; 57.8%; Pred. No. 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER APPLICATION NUMBER: 60/048,978
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
                                                                                                                                                                             EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,972
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: SITE
LOCATION: (1999)
CTHER INFRATION: n equals a,t,g, or US-09-205-258-171
                         FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,915
FILING DATE: 1997-06-06
                                                                                                      APPLICATION NUMBER: 60/049,019
FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCACACCCTTCCAGGCATTTGCC 83
APPLICATION NUMBER: 60/048,892
                                                                                                                                                            APPLICATION NUMBER: 60/048,970
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OTHER INFORMATION: n equals a,t,g,
                                                                                                                                     1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 171
LENGTH: 2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
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1155 GCCCGGCCAGCGTTTCGCTG 1135

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496 Grecargeceádeadeadeageceadecadadadagagagagagararecedagadeeedare 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/085,848
FILING DATE: 28-MAY-1998
CLASSIFICATION: 435
ATTOMNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REGISTRATION NUMBER: 32,837
REGISTRATION NUMBER: UM-03338
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 705-8318
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 220 MONTGOMERY STREET, SUITE 2200 CITY: SAN FRANCISCO STATE: CALLIFORNIA COUNTRY: UNITED STATES OF AMERICA
141 AGTCCGCCGATCAGCAGCGGCGCCATCAGGGA 172
                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, ILP
STREET: 220 MONTCOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-562-616-2/c
; Sequence 2, Application US/09562616
; Fatent No. 6599744
; GENERAL INFORMATION:
; APPLICANT: ASKARI, FREDERICK K.
TITLE OF INVENTION: IMPROVED VECTORS
; NUMBER OF SEQUENCES: 2
                                                                                                                                                           'atent No. oliveral
GENERAL INFORMATION:
APPLICANT: ASKARI, FREDERICK K.
APPLICANT: ASKARI, IMPROVED VECTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL,
                                                                                                                                                                                                                                                                                                                                                                 CITY: SAN FRANCISCO
STATE: CALLFORNIA
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "DNA"
                                                                                                                               Sequence 2, Application US/09085848 Patent No. 6171855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        436 ¢GGACACTTGTCCCCC 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 742 base pairs
TYPE: nucleic acid
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                                                                              RESULT 13
US-09-085-848-2/c
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Sequence 13956, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 13956
                                                                                                                                                     APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (1253); OTHER INFORMATION: Identity of nucleotide at the above locations are unknown. US-09-252-991A-15295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 GGGGGTCAGGCCCCAGCCGCGGGAAGCGCGCCCAGGAGCGCGCGAAACCTTCTCCACACCC 67
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Pred. No. 24;
0; Mismatches 41; Indels
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                                                                                                    Sequence 15295, Application US/09252991A
Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190 GCCCCGGCCAGCGTTTCGCTG 210
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ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
US-09-252-991A-13956
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                                                                                    US-09-252-991A-15295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 15295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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Gaps

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1182 AGTCCGCCGATCAGCAGGCGCGCATCAGGGA 1151
                                                                                                        Search completed: May 7, 2004, 15:44:40 Job time: 57.7167 secs
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Sequence 13604, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERGINGOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERGINGOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERGINGOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US/09/252,991A

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 GGGGGTCAGGCCCCAGGGAAGCGCGCCCAGGAGCGCGCGAAACCTTCTCCACACC 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 GTCAGGCCCCCAGCCGCGGAAGCGCGCCCAGGAGCGCGAAACCTTCTCCACACGTTC 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 742;
     MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/62,616
FILING DATE: 01-May-2000
CLASSIFICATION: CURNOWN>
PRIOR APPLICATION NUMBER: US/09/085,848
ATYORNEY/ACBNI THORMANTION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REPRENCE/DOCKET NUMBER: 32,837
REPRENCE/DOCKET NUMBER: UM-03338
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 705-8410
TELEPAX: (415) 37-8338
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
26.1%; Score 26.4; DB 4; Length 7.
Best Local Similarity 59.2%; Pred. No. 25;
Matches 45; Conservative 0; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 742 base pairs
TYPE: nucleic acid
STRANDENRES: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           436 cggacacrrcrcccc 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-09-252-991A-13604/c
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LENGTH: 2103
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68 CTTCCAGGCATTTGCCCGCCGCGATTCAGAGA 99

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(c) 1993 - 2004 Compugen Ltd.
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Post-processing: Minimum Match 0% Maximum Match 99% Listing first 45 summaries geneseqn2001as:*
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geneseqn2003as:* geneseqn2003bs:*
geneseqn2003cs:* N_Geneseq_29Jan04:* geneseqn1980s:* geneseqn1990s:* geneseqn2000s:* 198: Database :

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004s:*

	Description	Abt11173 Human 5	Abt11114 Human 5-1	Abl32117 Human imm	Abk31177 Signal tr	Abl70132 Chemicall	Abl32116 Human imm	Abk31176 Signal tr	Abl70131 Chemicall	Abk84481 Human cDN	Add14691 Human src	Aal50815 Human can	Abz59005 Human onc	Abz52368 Aspergill	Abz58996 Human onc	Abz58995 Human onc	Aac98960 Human pan	Abk15293 Ralstonia	Aba99469 Actinopla	Aat77840 Human mel	Aat12462 Human K+	Aav04874 cDNA sequ	Adc99154 Human mat	Ada57655 BAC fragm
SUMMARIES	QI	டி	ABT11114	ABL32117	ABK31177	ABL70132	ABL32116	ABK31176	ABL70131	ABK84481	ADD14691	AAL50815	ABZ59005	ABZ52368	ABZ58996	ABZ58995	AAC98960	ABK15293	ABA99469	AAT77840	AAT12462	AAV04874	ADC99154	ADA57655
	DB		ø	9	9	9	9	ø	9	9	σ	9	7	7	7	7	m	9	9	7	7	7	σ	7
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The invention relates to an isolated human nucleic acid molecule comprising an allelic variant of a polymorphic region of a 5-lipoxygenase (5-LO) gene, where the allelic variant comprises one or more nucleotide selected from any of 3, 20 or 21 base pair sequences, given in the specification, or their complement. The compositions and methods of the

New isolated nucleic acid molecule with an allelic variant of a polymorphic region of an 5-LO gene, useful for diagnosing and/or prognosticating disorders associated with an aberrant inflammatory

Disclosure; Fig 4; 290pp; English.

response such as asthma.

C 24 27.8 27.5 4456 7 ADA41527 C 25 27.8 27.5 14918 7 ADA526792 C 27 27.8 27.5 14918 7 ADA57654 C 28 27.8 27.5 14918 7 ADA57654 C 29 27.8 27.5 14918 7 ADA41526 3 2 27.8 27.5 14918 7 ADA41526 3 1 27.4 27.1 14918 9 ADC74633 3 2 27.4 27.1 744 4 AAK91239 3 4 27.2 26.9 326 4 AAK31240 3 5 27.2 26.9 326 4 AAK31265 3 6 27.2 26.9 326 6 ABA6675 3 7 26.7 26.9 326 6 ABA6675 3 8 27.2 26.9 326 6 ABA6677 4 1 27 26.7 615 6 ABA63316 C 40 27 26.7 615 6 ABA63316 C 41 27 26.7 615 6 ABA63316 C 42 27 26.7 615 6 ABA63354 C 43 27 26.7 2033 8 ACH44855 C 44 27 26.7 2003 8 ACH44665	Ada41527 Human sec	Adc74634 Human sec		Ada57654 BAC fragm	Ada41526 Human sec	Abx74141 Human nov	Adc74633 Human sec	Human	Aak91239 Human dig	Aak91240 Human dig	Aba06675 Human cDN	Aas31605 cDNA enco	Abv84012 Human pol	Add47395 Rat gene	Aca35947 Prokaryot	Abq53011 Oligonucl		Aax04400 Human sec	Aav84571 Human sec	Aba83354 Human sec	Ach04855 Novel hum	Acd44665 Human cDN
24 27.8 27.5 4456 25 27.8 27.5 4456 27 27.8 27.5 14918 28 27.8 27.5 14918 30 27.8 27.5 14918 31 27.4 27.1 1217 32 27.4 27.1 7640 33 27.4 27.1 7640 34 27.2 26.9 326 36 27.2 26.9 326 37 27.2 26.9 570 38 27.2 26.9 570 39 27.2 26.9 570 40 27 26.7 615 41 27 26.7 615 42 27 26.7 615 43 27 26.7 26.7 615 44 27 26.7 26.7 615	ADA41527	ADC74634	AAS26792	ADA57654	ADA41526	ABX74141	ADC74633	AAI59411	AAK91239	AAK91240	ABA06675	AAS31605	ABV84012	ADD47395	ACA35947	ABQ53011	ABQ53010	AAX04400	AAV84571	ABA83354	ACH04855	ACD44665
25 27.8 27.8 27.5 27.8 27.5 27.8 27.8 27.5 27.8 27.8 27.5 27.8 27.8 27.5 27.8 27.8 27.5 27.8 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5	7	σ	4	7	7	7	σ	4	4	4	4	4	ø	σ	7	9	9	N	N	4	ω	ω
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ALIGNMENTS

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Human, polymorphic region; 5-lipoxygenase; 5-LO gene; asthma; bronchitis; sinusitis; ulcerative colitis; nephritis; amyloidosis; sarcoidosis; hemmatoid arthritis; scleroderma; lupus; non-allergic rhinitis; polymyositis; Reiter's syndrome; psoriasis; pelvic inflammatory disease; atopic; contact dermatitis; forensic medicine; paternity testing; enzyme;
                                                                                   Human 5-lipoxygenase gene related DNA sequence SEQ ID No 63.
                      ABT11173 standard; DNA; 168174 BP
                                                                                                                                                                                                                                                                 08-FEB-2001; 2001US-0267515P.
21-AUG-2001; 2001US-0314248P.
                                                                                                                                                                                                                                            07-FEB-2002; 2002WO-US003546.
                                                                                                                                                                                                                                                                                                (MILL-) MILLENNIUM PHARM INC.
                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                          WPI; 2002-627522/67.
                                                                                                                                                                                                                                                                                                                     Meyer J;
                                                                                                                                                                                                    WO200262825-A2.
                                                                                                                                                                                 Homo sapiens.
                                                              05-DEC-2002
                                                                                                                                                                                                                        15-AUG-2002.
                                                                                                                                                                                                                                                                                                                     Barnes G,
                                          ABT11173;
RESULT 1
            ABT11173
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present invention are useful for diagnosing and/or prognosing disorders associated with an aberrant inflammatory response such as asthma, bronchitis, simusitis, ulcerative colitis, nephritis, amyloidosis, rheumatoid arthritis, sarcoidosis, soleroderma, lupus, non-allergic rhinitis, polymyositis, Reiter's syndrome, psoriasis, pelvic inflammatory disease, atopic and contact dermatitis. The nucleic acid molecules can also be useful for identifying an individual amongst other individuals from the same species for use in forensic medicine and paternity testing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lipoxygenase (5-LO)
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Sequence 168174 BP; 46808 A; 36442 C; 36942 G; 46474 T; 0 U; 1508 Other;

1; Length 168174; Indels ö Score 89; DB 6; Pred. No. 7.6e-17; 0; Mismatches 88.1%; 99.0%; Conservative Local Similarity Matches 100; Query Match

1 GGAACCTGGGGGTCAGGCCCCAGCCGCGGAAGCGCCCCAGGAGCGCGCGAAACCTTCT

à

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167319 GGAACCTGGGGGTCAGGCCCCAGCCGGGAAGC-CGCCCAGGAGCGCGCGAAACCTTCT 167377 61 d ⋩ 셤

167378 ccacaccerrecaddearridecedecederreadadad 167418

ABT11114 standard; DNA; 168273 RESULT 2

ABI11114;

(first entry)

05-DEC-2002

BP

Human 5-lipoxygenase gene related DNA sequence SEQ ID No 2.

Human, polymorphic region, 5-lipoxygenase, 5-LO gene, asthma, bronchitis, sinusitis, ulcerative colitis, nephritis; amyloidosis; sarcoidosis; hebumatoid arthritis, scleroderma, lupus, non-allergic rhinitis, polymyositis, Reiter's syndrome; psoriasis; pelvic inflammatory disease, atopic, contact dermatitis; forensic medicine; paternity testing; enzyme,

Homo sapiens.

WO200262825-A2

15-AUG-2002

07-FEB-2002; 2002WO-US003546

08-FEB-2001; 2001US-0267515P 21-AUG-2001; 2001US-0314248P

(MILL-) MILLENNIUM PHARM INC

Meyer J; Barnes G, WPI; 2002-627522/67

New isolated nucleic acid molecule with an allelic variant of a polymorphic region of an 5-LO gene, useful for diagnosing and/or prognosticating disorders associated with an aberrant inflammatory response such as asthma.

Disclosure, Fig 2; 290pp; English.

comprising an allelic variant of a polymorphic region of a 5-lipoxygenase (5-LO) gene, where the allelic variant comprises one or more nucleotide selected from any of 3, 20 or 21 base pair sequences, given in the specification, or their complement. The compositions and methods of the present invention are useful for diagnosing and/or prognosing disorders The invention relates to an isolated human nucleic acid molecule

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167476
               bronchitis, sinusitis, ulcerative colitis, nephritis, amyloidosis, rheumatorid arthritis, sarcoidosis, scleroderma, lupus, non-allergic rhimitis, polymyositis, Reiter's syndrome, psoriasis, pelvic inflammatory disease, atopic and contact dermatitis. The nucleic acid molecules can also be useful for identifying an individual amongst other individuals from the same species for use in forensic medicine and paternity testing. This polymucleotide sequence represents DNA relating to the human 5-lipoxygenase (5-LO) gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                              167418 GGAACTGGGGGTCAGGCCCCGGGGAAGC-CGCCCAGGAGCGCGCGAAACCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                    1 GGAACCTGGGGGTCAGGCCCCCAGCCGCGGAAGCGCCCCAGGAGCGCGCGAAACCTTCT
                                                                                                                                                                                                                                              Sequence 168273 BP; 46834 A; 36467 C; 36966 G; 46498 T; 0 U; 1508
such as asthma,
                                                                                                                                                                                                                                                                                                Length 168273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167477 ccacaccerrecaggearrrecegeegerreagagage 167517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 CCACACCCTTCCAGGCATTTGCCCGCGCGATTCAGAGAGC 101
                                                                                                                                                                                                                                                                                             88.1%; Score 89; DB 6; 1
99.0%; Pred. No. 7.6e-17;
ive 0; Mismatches 0;
associated with an aberrant inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABL32117 standard; DNA; 13249
                                                                                                                                                                                                                                                                                                                                                  100; Conservative
                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                     Matches
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ABL32117;

(first entry) 26-MAR-2002 Human immune system associated gene SEQ ID NO: 90.

antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS, epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene; Human; immune system disease; cytosine methylation; antiasthmatic;

Homo sapiens.

WO200200928-A2

03-JAN-2002

02-JUL-2001; 2001WO-EP007537

2000DE-01032529. 2000DE-01043826. 01-SEP-2000; 30-JUN-2000;

(EPIG-) EPIGENOMICS AG

Berlin K; ບັ Piepenbrock Olek A,

WPI; 2002-130909/17

chemically modified gene, useful for associated with abnormal cytosine fragment of of diseases Nucleic acid comprising diagnosis and treatment methylation.

Claim 1; SEQ ID NO 90; 32pp + Sequence Listing; German.

The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,

specification, but was obtained in electronic format directly from the European Patent Office

Sequence 13249 BP; 3128 A; 273 C; 3397 G; 6451 T; 0 U; 0 Other;

1;

Gaps

1;

Length 13249; 20; Indels

Score 55; DB 6; Pred. No. 7.8e-07 0; Mismatches

54.5%;

Query Match
Best Local Similarity 78.0.

62

9089 AACCTAAAATCAAACCCCAACCGCGAAAAC-CGCCCAAAACGCGCGAAACCTTCTCC 9031

3 AACCTGGGGGTCAGGCCCCAGCGGGGAAGCGCGCCCAGGAGCGCGCGAAACCTTCTCC

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                                                                                                                                                                             9089 AACCTAAAATCAAACCCCAACCGGAAAAAC-GGCCCAAAAACGGGGAAACCTTCTCC 9031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to chemically modified DNA sequences of signal transduction associated genes. The DNA sequences are chemically modified using a solution of bisulphite, bydrogen sulphite or disclosed are oligonucleotides and/or DNA oligomers for detecting the cytosine methylation state (CpG islands) of these genes, and a method for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with signal transduction. The genomic DNA can be obtained from cells or cellular components which contain DNA, e.g. cell lines, biopsies, blood sputum, stool, urine, cerebral-spinal fluid, tissue embedded in parafin such as tissue from eyes, intestine, kidney, and all their possible combinations. The sequences of the invention are useful for the diagnosis and therapy of diseases associated with signal transduction e.g. solid tumours and cancer. ABR31159-ABR31545 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; signal transduction associated gene; cytosine methylation state; CpG island; signal transduction associated disease; solid tumour; cancer; antitumour; cytostatic; mutant; ds.
                                                                                                                                                   62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligonucleotide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic sequences of genes associated with signal transduction.
                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal transduction associated gene modified complementary DNA #10.
psoriasis and inflammatory/ulcerative bowel sequence is a gene of the invention
                                                                                                                  1;
                                                Sequence 13249 BP; 3128 A; 273 C; 3397 G; 6451 T; 0 U; 0 Other;
                                                                                 Length 13249;
                                                                                                                  20; Indels
                                                                                                                                                                                                                                               9030 ACACCCTTCCAAACATTTACCCGCGCGATTCAAAAAC 8992
                                                                                                                                                                                                                63 ACACCCTTCCAGGCATTTGCCCGCGCGATTCAGAGAGC 101
                                                                                 Score 55; DB 6;
Pred. No. 7.8e-07;
                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ID NO 20; 24pp; English.
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                                                                                                                                                                                                                                                                                                                                 BP
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                                                                              54.5%;
78.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JUN-2000; 2000DE-01032529
01-SEP-2000; 2000DE-01043826
                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                Query Match
Best Local Similarity 78.0%
Local Similarity 78.0%
T8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (EPIG-) EPIGENOMICS AG.
rheumatoid arthritis,
diseases. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-147896/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200200926-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                  23-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
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                                                                                                                                                                                                                                                                                                                  ABK31177,
                                                                                                                                                                                                                                                                                                  RESULT 4
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SSXSS
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The invention relates to a nucleic acid comprising a sequence of at least 18 bases of a segment of chemically pretreated DNA of genes associated with cell signalling. The activity of the modified sequences of the invention may be described as cytostatic. The object of the invention is considerable to the invention is signalling, as well as oligonucleotides and/or PNA-oligoners for cetecting cytosine methylations, as well as a method which is particularly suitable for the diagnosis and/or therapy of genetic and cepigeneric parameters of genes associated with cell signalling. The chemically modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as solid tumours and cancer. The sequences given in records ABL7011-ABL70626 represent chemically pre-treated genomic DNA's of genes associated with cell signalling. Note: The sequence data for this patent is not represented in the printed sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the
                                                                                                                                                                                                                                                                                                    signalling; cytosine methylation; cell signalling disease; cancer;
nr; cytostatic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signaling e.g. cancer, comprises chemically modified genomic sequences of genes associated with cell signaling.
                                                                                                                                                                                                                                                              Chemically treated cell signalling DNA sequence complementary to#11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13249 BP; 3128 A; 273 C; 3397 G; 6451 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 22; 24pp + Sequence Listing; English.
                             9030 ACACCCTTCCAAACATTTACCCGCCGCGGATTCAAAAAC 8992
63 ACACCCTTCCAGGCATTTGCCCGCCGCGATTCAGAGAGC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Berlin K;
                                                                                                                                         BP.
                                                                                                                                     ABL70132 standard; DNA; 13249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUN-2001; 2001WO-EP007471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUN-2000; 2000DE-01032529.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-SEP-2000; 2000DE-01043826
                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Suropean Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EPIG-) EPIGENOMICS
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                                                                                                                                                                                                                                                                                                                                                                                                        WO200202807-A2.
                                                                                                                                                                                                                                                                                                                                                                  Unidentified
                                                                                                                                                                                                                      01-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                              10-JAN-2002
                                                                                                                                                                                ABL70132;
                                                                                                                                                                                                                                                                                                                              tumour;
                                                                                                                    ABL70132/c
                                                                                               RESULT 5
                                 qq
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chemically pretreated genomic DNA sequences of different genes associated with signal transduction, or their complementary sequences. Note: The sequence data for this patent did not form part of the printed

4

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The present invention provides a number of human immune system associated dense which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid rebuxaemia, Alzheimer's disease, Alz, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
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                                                                                                             9031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for
                                                                                62
                                                                                                                                                                                                                                                                                                                                                                                                          antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                        9089 AACCTAAAAATCAAACCCCAACCGCGAAAAAC-CGCCCAAAAAGGCGCGAAACCTTCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytosine
                                                                                3 AACCTGGGGGTCAGGCCCCAGGGGGGGGCGCCCAGGAGCGCGCGAAACCTTCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified gene, useful with abnormal cytosine
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                            immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13249 BP; 3594 A; 273 C; 3130 G; 6252 T; 0 U; 0 Other;
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               Length 13249;
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Pred. No. 0.0026;
0; Mismatches 28; Indels
                                              20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 89; 32pp + Sequence Listing; German.
                                                                                                                                                                              9030 ACACCCTTCCAAACATTTACCCGCCGCGATTCAAAAAC 8992
                                                                                                                                                63 ACACCCTTCCAGGCATTTGCCCGCCGCGATTCAGAGAGC 101
                                                                                                                                                                                                                                                                                                                                                               Human immune system associated gene SEQ ID NO: 89.
               Score 55; DB 6;
Pred. No. 7.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fragment of chemically of diseases associated
                                              0; Mismatches
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                                                                                                                                                                                                                                                             ABL32116 standard; DNA; 13249 BP.
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               54.5%;
78.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-SEP-2000; 2000DE-01043826
                                                                                                                                                                                                                                                                                                                                (first entry)
                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid comprising
diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EPIG-) EPIGENOMICS AG
Query Match
Best Local Similarity
Thes 78; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-130909/17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          methylation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                ABL32116;
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The present invention relates to chemically modified DNA sequences of signal transduction associated genes. The DNA sequences are chemically modified using a solution of bisulphite, hydrogen sulphite or disculphite. Also disclosed are oligonocletides and/or PNA oligomers for detecting the cytosine methylation state (CpG islands) of these genes, and a method correct associated with signal transduction. The genomic DNA can method genes associated with signal transduction. The genomic DNA, e.g. cell contained from cells or cellular components which contain DNA, e.g. cell contain, heart, prostate, lung, breast or liver, histologic object slides, brain, heart, prostate, lung, breast or liver, histologic object slides, cuseful for the diagnosis and therapy of diseases associated with signal transduction e.g. solid tunnours and cancer. ABK31158-ABK31545 represent chemically pretreated genomic DNA sequences of different genes associated with signal transduction, or their complementary sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4159 GGAATTTGGGGGTTAGGTTTTAGTCGCGGGAAG-TCGTTTAGGAGCGCGCGAAATTTTTT 4217
                                                                                                                                                                                                                                                                                             Human, signal transduction associated gene, cytosine methylation state, CpG island, signal transduction associated disease, solid tumour, cancer, antitumour, cytostatic, mutant, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oligonucleotide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic sequences of genes associated with signal transduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13249 BP; 3594 A; 273 C; 3130 G; 6252 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 43.2; DB 6; Length 13249;
Pred. No. 0.0026;
0; Mismatches 28; Indels 1;
                                     4218 Trararritraskirarrikarrikarkikarrikakak
61 CCACACCCTTCCAGGCATTTGCCCGCGCGATTCAGAGAG 100
                                                                                                                                                                                                                                                          Signal transduction associated gene modified DNA #10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 19; 24pp; English.
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                                                                                                                                      BP.
                                                                                                                                      ABK31176 standard; DNA; 13249
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71.0%;
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01-SEP-2000; 2000DE-01043826.
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Best Local Similarity 71.0
Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Olek A, Piepenbrock C,
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                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                              ABK31176
                                                                                                 RESULT 7
                                                                                                                      ABK31176
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Gaps

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Local Similarity 71.0 es 71; Conservative

Matches

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4217

4159 GGAATTIGGGGGTIAGGTTTIAGICGCGGGAAG-TCGTTIAGGAGCGCGCGAAATTTTTT

Tue May 11 11:56:46 2004

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The invention relates to a nucleic acid comprising a sequence of at least

18 bases of a segment of chemically pretreated DNA of genes associated

25 with cell signaling. The activity of the modified sequences of the

26 invention may be described as cytostatic. The object of the invention is

27 invention may be described as cytostatic. The object of the invention is

28 signalling, as well as oligonucleotides and/or PNA-oligomers for

28 detecting cytosine methylations, as well as a method which is

29 particularly suitable for the diagnosis and/or therapy of genetic and

29 epigenetic parameters of genes associated with cell signalling. The

20 chemically modified DNA provided by the invention is useful for diagnosis

20 chemically modified DNA provided by the invention is useful for diagnosis

21 and therapy of diseases such as solid tumours and cancer. The sequences

21 grown in records ABL70111-ABL70626 represent chemically pre-treated

22 genomic DNA's of genes associated with cell signalling. Note: The

23 sequence data for this patent is not represented in the printed

24 specification, but is based on sequence information supplied by the

25 Buropean Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell signalling; cytosine methylation; cell signalling disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signaling e.g. cancer, comprises chemically modified genomic sequences of genes associated with cell signaling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GGAACCTGGGGGTCAGGCCCCAGCGGGGAAGCGCGCCCAGGAGCGCGCGAAACCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 21; 24pp + Sequence Listing; English.
                                               4218 TIAIATITITITIAGGIAITITGITCGICGCGAITIAGAGAG 4257
61 CCACACCCTTCCAGGCATTTGCCCGCCGCGATTCAGAGAG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chemically treated cell signalling DNA sequence#11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Berlin K;
                                                                                                                                                                                                                                                              ABL70131 standard; DNA; 13249 BP.
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01-SEP-2000; 2000DE-01043826.
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71.0%;
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Best Local Similarity 71.0
Matches 71; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumour; cytostatic; ds.
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ABL70131

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4159 GGAATTIGGGGGTTAGGTTTTAGTCGCGGGAAG-TCGTTTAGGAGCGCGCGCAAATTTTTT 4217

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4218 TTATATTTTTTAGGTATTTGTTCGTCGCGATTTAGAGAG 4257

61 CCACACCCTTCCAGGCATTTGCCCGCCGCGATTCAGAGAG 100

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The invention relates to detecting (MI) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (GS) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of GS is indicative of GCA. Also included are modulating (M2) GA by contexting GC with an agent that alters the expression of at least one gene in GS; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue or sterile inflammatory disease using the gene expression of subject to a pathogen or sterile inflammatory disease using the gene expression of the seponse in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from GS, where the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammatory disease, by contacting a tissue having inflammation with an agent that modulates the expression of gene (s) from GS, where the level of inflammatory disease, by contacting a tissue having inflammation with an agent that modulates the expression of gene (s) from GS in the tissue M1 is useful for modulating GA, M3 is useful cor secenting an agent capable of modulating GA preferably in an inflammation in a tissue, M4 is useful for modulating GA, M3 is useful correcting an inflammation and arthritis, glomerulonebritis, asthma, thrombosis, cardiac reperfusion injury, renal reperfusion injury, ARDS, adult correspondent allowance, inflammatory disease, confirst and reperfusion injury, renal reperfusion injury, arrivance is a cardiac reperfusion injury, renal reperfu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity.
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                                                                                                                                                                                                                                                     Human; ss; granulocytic cell; DNA chip; bacterial infection, viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                                                                                                                                                                                                         Human cDNA differentially expressed in granulocytic cells #1052.
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                                                 ABK84481 standard; cDNA; 44147 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beazer-Barclay Y, Weissman SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-OCT-2001; 2001WO-US030821.
                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-435328/46.
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                                                                                                    ABK84481;
                        ABK84481/c
RESULT 9
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The present invention describes a predictor set comprising a plurality of polynucleotides or polypeptides whose expression pattern is predictive of the response of cells to treatment with a compound that modulates protein tyrosine kinase activity or members of the protein tyrosine kinase activity of cells, comprising obtaining a sample of modulating the activity of cells, comprising obtaining a sample of cells, correlating the expression of the markers to the compound's ability to modulate the activity of the cells; (2) a plurality of eall lines for modulate the activity of the cells; (2) a plurality of cell lines for correlate with compound sensitivity or resistance of cells associated with a disease state; and (3) identifying polynucleotides and collypeptides that predict compound sensitivity or resistance of cells associated with a disease state, comprising subjecting the plurality of cell lines to one or more compounds, analysing the expression pattern of
                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         predictor set; protein tyrosine kinase activity modulator;
protein tyrosine kinase pathway; protein tyrosine kinase; cytostatic;
gene therapy; drug sensitivity; genetic profile; cancer; human; gene; ss.
                                                                                                                                                                                                                 89
expressed in granulocytes. Note: The sequence data for this patent did
                                                                                                                                                                                                               9 GGGGTCAGGCCCCAGGGGGGAAGCGCCCCAGGAGCGCGCGAAACCTTCTCCACACCC
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotides and polypeptides for predicting the activity of compounds that interact with protein tyrosine kinases and/or protein
                                                                                                        Other;
                                                                                                                                                                              ;
                              not form part of the printed specification, but was obtained electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                    Sequence 44147 BP; 9813 A; 11709 C; 11789 G; 10833 T; 0 U; 3
                                                                                                                                        Score 30; DB 6; Length 44147;
Pred. No. 26;
0; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human src biomarker polynucleotide SEQ ID NO:85.
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                                                                                                                                                                                                                                                                                     TTCCAGGCATTTGCCCGCCGCGATTC
                                                                                                                                                                                                                                                                                                                                                                                                               ADD14691 standard; cDNA; 44147 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                        29.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tyrosine kinase pathways.
                                                                                                                                                                            51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Huang F, Fairchild CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2003-636735/60.
                                                                                                                                                         Local Similarity
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                                                                                                                                            Query Match
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polynucleotides or polypeptides that predict the sensitivity or resistance of cells associated with a disease state by using the expression pattern of the microarray. The polynucleotides and polypeptides have cytostatic activities, and can be used in gene therapy. The polynucleotides are useful in predicting the activity of compounds that interact with protein tyrosine kinases and/or protein tyrosine kinase pathways. These may be used in determining drug sensitivity in patients to allow the development of individualized genetic profiles which aid in treating diseases and disorders (e.g. cancer) based on patient response at a molecular level. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nter-aided statistical method for predicting cancer, applicable in
therapy for evaluating cancer malignancy with data for use in drug
                                                                                                                                                                                                                                                                                                                                               9 GGGGTCAGGCCCCAGGGGGGAAGCGCCCAGGAGCGCGCGAAACCTTCTCCACACC
                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                  Sequence 44147 BP; 9813 A; 11709 C; 11789 G; 10833 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, gene therapy, cancer status prediction, cancer, ds, cancer malignancy evaluation, drug design, antisense nucleic acid
                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cancer status prediction method-related DNA sequence #7
                                                                                                                                                                                                                                                                     29.7%; Score 30; DB 9; Length 44147; 59.3%; Pred. No. 26; ive 0; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 132-152; 182pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            29298 cedeccédecrirécraécédadecric 29273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matoba R;
                                                                                                                                                                                                                                                                                                                                                                                                                        94
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HITACHI SOFTWARE ENG CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                        69 TTCCAGGCATTTGCCCGCCGCGATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
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ID AAL50815 standard; DNA; 33737
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06-APR-2001; 2001JP-00108503.
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                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                     Local Similarity
nes 51; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Iwao K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200272828-A1.
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                                                                                                                                                                                                                                                                       Query Match
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(HISF )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        design.
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microarray of polynucleotides or polypeptides, and selecting

fermentation; fungus; industrial; EST;

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Aspergillus oryzae polynucleotide SEQ ID NO 1481
                                                                                                                                                                                                                                                                               expressed sequence tag; gene; ss.
                                                                                    ABZ52368 standard; cDNA; 990 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAR-2001; 2001JP-00098371.
                                                                                                                                                                                                                                                         Aspergillus oryzae;
                                                                                                                                                                                                                                                                                                                       Aspergillus oryzae
                                                                                                                                                                                                                                                                                                                                                                 WO200279476-A1.
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                                                                                                                                                                    28-MAR-2003
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                                                                                                                              ABZ52368;
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                                                                  ABZ52368/c
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                                          RESULT 13
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                                                                                                                                                                    0;
                                                                                                                                                                                                                                       8876 GGCTCAGGGCTCCAGGCGCCCCCAGACGCCCCAGGGCAGCCCTCCACCCTCCACCTCCACCTCCTCCT 8817
                                                                                                                                                                                                                 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40 cecesceses de consecuence de consecuencia d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oncosuppressive; apoptotic; p53; p73; cytostatic; gene therapy; tumour;
                                                                                                                                                                                                              10 GGGTCAGGCCCCAGCCGCGGGAAGCGCCCCAGGAGCGCGCGAAACCTTCTCCACACCT
                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to oncosuppressive polypeptides and encoding polynuclectides. The oncosuppressive gene is involved in apoptotic process and is regulated by p53 and p73. The oncosuppressive polynuclectides are useful for preparing a medicament for treating tumour. The present sequence represents a human oncosuppressive gene (DRAGO) fragment regulating the expression of the polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New oncosuppressive polypeptide, useful for preparing a medicament
(e.g. antisense nucleic acids for use in ). The present DNA sequence represents a
                                                                                  Sequence 33737 BP; 8084 A; 9254 C; 8733 G; 7663 T; 0 U; 3 Other;
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                                                                                                                            Length 33737;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35; Indels
                                                                                                                                                                    Indels
                                                                                                                                                                    21;
                                                                                                                            DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human oncosuppressive gene (DRAGO) fragment.
                                                                                                                        29.1%; Score 29.4; D
llarity 66.7%; Pred. No. 37;
Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 42; 42pp; English.
for use in drug design (e.g. a
therapy to treat cancer). The
nucleic acid of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DRAGO; human; gene; ds
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Matches 50; Conser
                                                                                                                                         Local Similarity
hes 42; Conserv
                                                                                                                                                                                                                                                                                                                                           8816 ACC 8814
                                                                                                                                                                                                                                                                                                 TCC 72
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                                                                                                                          Query Match
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ABZ59005
ID ABZ59
                                                                                                                                                                  Matches
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88338
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The invention relates to a polynucleotide having any of 6006 specific sequences (ABZ50888-ABZ56893), which are expressed by a fungus under specific outlure conditions including one or more of eutrophic, oligotrophic, solid, early germination, alkaline, high temperature, low temperature or maltose culture or polynucleotides stringently hybridising progress of fermentation and the growth conditions of a fungus, especially of Aspergillus oryzes which is widely used in industrial fermentation. Also monitoring for fungal contamination. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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                                                                                                                                                                                                                                                                                                            monitoring the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   467 GTCCCAGGCGCCGGAAGCAGGCACGCAGCCTGCCAAACCTGCCGCACATCTGCGACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 GCCCCAGCCGCGCGCGCCCCAGGAGCGCGCGAAACCTTCTCCACACCTTCCAGGC
                                                                                                                                                                                                                                                                                                     Detection of expression of specific Aspergillus genes for monitorir fermentation and growth conditions of the fungus, using DNA probes.
                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 1481; 48pp + Sequence Listing; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.7%; Score 29; DB 7; Length 990; 58.8%; Pred. No. 33; ive 0; Mismatches 35; Indels
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                                                                                                                                    Horiuchi
                                                                                                                                                                       Abe K;
                                                                                                                                    Akita O, Kashiwagi Y, Kitamoto K, Kobayashi T, Kitamoto N, Gomi K,
INST ADVANCED IND SCI & TECHNOLOGY
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                                  (NARE-) NAT RES INST BREWING.
(NORQ ) NAT FOOD RES INST MIN AGRIC.
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      NAAD-) NAT
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                                                                                                                                 Machida M,
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5 CCTGGGGGTCAGGCCCCAGCCGGGGAAGCGCGCCCAGGAGCGCGCGAAACCTTCTCCAC 64
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                                                                                                                                                                                                                                                                                                                            Score 29; DB 7; Length 3761;
Pred. No. 38;
0; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human oncosuppressive gene (DRAGO) fragment.
                 Human oncosuppressive gene (DRAGO) fragment
                                                                                                                                                                                                                                                                                                                                                                                                              105 CCTTTCCCGCCCTTCCCCGCCC 129
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                                                                                                                                                                                                                              Claim 3; Page 37-38; 42pp; English
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                                                                                                                09-JUL-2002; 2002WO-EP007625.
                                                                                                                                10-JUL-2001; 2001IT-MI001465.
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 58.8%;
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                  Broggini M, D'incalci M;
                                                                                                                                                 (NOVU-) NOVUSPHARMA SPA
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                                                                                                                                                                                   WPI; 2003-221715/21
                                                                                                                                                                                                                                                                                          (DRAGO) fragment
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                                                             Homo sapiens.
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ABZ58995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Page 34-37; 42pp; English
                                                                                                  Broggini M, D'incalci M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 28.7
Best Local Similarity 58.8
Matches 50; Conservative
(NOVU-) NOVUSPHARMA
                                                                                                                                                                                                               WPI; 2003-221715/21
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                                                                                                                                                                                                                                                                                                                                                                                             treating tumors
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                                                                                                                                                                                                    Oncosuppressive, apoptotic; p53; p73; cytostatic; gene therapy; tumour; DRAGO; human; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New oncosuppressive polypeptide, useful for preparing a medicament for treating tumors:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to oncosuppressive polypeptides and encoding polymuclectides. The oncosuppressive gene is involved in apoptotic process and is regulated by p53 and p73. The oncosuppressive polymuclectides are useful for preparing a medicament for treating tumour. The present sequence represents a human oncosuppressive gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3761 BP; 800 A; 968 C; 991 G; 1002 T; 0 U; 0 Other;
     (first entry)
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0;

Gaps

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ם מייים						
ו ט	. Score	Match	Length	DB	ID	Description
	1 8	88.1	12926	9	7315	731567 Human DI
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υ	Ω.	54.5	1324	9	4	4173 Sequen
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	43.	42.8	1324	9	8	3563 S
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<u> </u>	.0 35	34.7	258227	7	AC106376	AC106376 Rattus no
	. 3	34.7	30704	0	AC130592	1592
U	2 34.	34.1	19947	(7	AC093452	3452
	32.	31.9	25354	7	AC093960	3960
U U	32.	31.9	25734	N	AC111855	852
	m G	31.7	1255	Н	AE001980	1980
	6 31.	31.3	9751	C)	AC091670	167
U U	7 31.	31.3	13388	σ	AC133334	3334
	8 31.	31.1	12842	~	AC144889	1889
Н	31.	31.1	25126	N	AC145193	5193
ט	e 0	30.7	9017	σι	HSDJ858B6	3511 Humar
	1 30.	30.5	32553	~	AC125699	5699 Rattu
C4	2 30.	30.1	17112	7	AC142009	2009 Rattus
0	3 30.	30.1	18178	7	AC116970	5970 Rattus
23	4 30.	30.1	18902	10	AL831754	31754 Mous
U	30.	30.1	18912	σ	AC073094	3094 Homo sa
	6 30.	29.9	12441	σ	AL354919	1919 Huma
C4	7 30.	29.9	18324	71	AC129965	3965 Sus
	8 30.	29.9	19111	9	AC068629	362
	6	29.7	4414	σ	HSU93305	35 Homo s
е С	6	29.7	14033	σ	AF235097	5097 Homo
	1	29.7	18399	σ	AF196779	5779 HOM
	3	29.7	22563	7	AC125294	5294 Ratt
	3 29.	29.5	88	Н	AF239240	9240 Rals
	4 29.	29.5	259	σ	AB067772	7772 Homo
m	5 29.	29.5	302	σ	BC048428	3428 Homc
e	6 29.	29.5	1192	н	AE005111	5111 Halo
υ υ	7 29.	29.5	9699	~	AC095759_3	inuation
c	8 29.	29.5	11000	7	265	inuation
9	9 29.	29.5	14009	σ	AL162615	52615 Huma
4	0 29.	29.5	19305	1	AL646062	46062 Rals
Ω	1 29.	29.5	19605	Н	46	46058
4	2 29.	29.5	21505	-	46	46084 Ralstoni
4	3 29.	29.5	21605	~;	46	46076 Ralstoni
4	4 29.	29.5	22005	Н	46	46074 Ralstoni
•		000	30100	¢	C	Olo Domo san

ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1 AL731567 LOCUS DEFINITION

ALIGNMENTS

AL731567 129266 bp DNA linear PRI 20-JUN-2002

NO Human DNA sequence from clone RP11-67C2 on chromosome 10, complete sequence

Sequence AL731567 AC010865

NAT731567 AC010865

HTG.

Homo sapiens (human)

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

Mintehead, S.

Direct Submission REFERENCE AUTHORS TITLE

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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Brown, J., Castlefa, C., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Castlefano, K., Dowar, K., Collymore, A., Cooke, P., Darellano, K., Dewar, K., Comino, M., Donelan, L., Doyle, M., Perreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyra, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Horton, L., McEwan, P., McGernan, K., Mcdenald, P., Marquis, N., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McKernan, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Subramanian, A., Talamas, J., Ranger-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tasfaye, S., Tinrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M. Oo, A., Wheeler, J., Wu, X., Wyman, D., Ya, J., Subramanian, A., Wesearch, 320 Charles Street, Cambridge, MA 02141, USA On Mar 14, 2000 this sequence version replaced gi:6524208.

All repeats were identified using RepeatMasker.

Smit, A. F. A. & Green, P. (1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arbitrary, daps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 30 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality coverage: 2.9 in Q20 bases; agarose-fp Quality coverage: 3.0 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
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gap of 100 bp
contig of 1509 bp in length
gap of 100 bp
contig of 1209 bp in length
gap of 100 bp
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of 2712 bp in length
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18183
20524
            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
                                                                                                                                                    buring sequence assembly data is compared from overlapping clones. Buring, //www.genomecorp.com
During sequence assembly data is compared from overlapping clone have differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw:, SMISSERCT; Tr:, TREMBL; Wp:, WORNPERP; Information on the WORNPEPP database can be found at the feature table with their source databases: Em: Chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Ruther information can be found at http://www.sanger.ac.uk/HGPP/Chr10 RPI1-67C2 is from the library RPC1-11.1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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Homo sapiens clone RP11-16P14, WORKING DRAFT SEQUENCE, 30 unordered
pieces.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 160654)
            Submitted (31-MAY-2002) Wellcome Trust Sanger Institute, Hinxton,
                               Cambridgeshire, CB10 1SA, UK. B-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequestGeanger.ac.uk
On Jun 21, 2002 this sequence version replaced gi:21213582.
Braft Sequence Produced by Genome Therapeutics Corp, 100 Beaver
Street, Waltham, MA 02453, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.1%; Score 89; DB 9; Length 129266; 99.0%; Pred. No. 1.7e-13; rive 0; Mismatches 0; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33746 CCACACCCTTCCAGGCATTTGCCCGCCGCGATTCAGAGAGC 33786
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Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="10"
/clone="RR11-67C2"
/clone_lib="RPCI-11.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC011879.3 GI:7239554
HTG; HTGS PHASE1; HTGS_DRAFT.
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VECTOR: pBACe3.6.
Location/Qualifiers
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Best Local Similarity
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               JOURNAL
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Diagnosis of diseases associated with signal transduction
Patent: WO 0200926-A 20 03-JAN-2002;
Epigenomics AG (DE)
Location/Qualifiers
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Sequence 20 from Patent WO0200926.
AX344173
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1. 151
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252. .1760
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Diagnosis of diseases associated with the immune system
Patent: WO 0200928-A 90 03-JAN-2002;
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Pred. No. 0.00017;
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1. 13249
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78.8%; Pred. No. o...
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Sequence 22 from Patent W00202807.
AX348564
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Sequence 90 from Patent WO0200928.
AX345019
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Location/Qualifiers
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                                       9089 AACCTAAAAATCACCCCAACCGGGAAAAAC-CGCCCAAAAAGGGGGGAAACCTTTCTCC 9031
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3 AACCTGGGGGTCAGGCCCCAGCGGGGAAGCGCCCCAGGAGCGCGCGAAACCTTCTCC
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Diagnosis of diseases associated with signal transduction
Patent: WO 0200926-A 19 03-JAN-2002;
Epigenomics AG (DE)
Location/Qualifiers
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/mol_type="unassigned DNA"
_db_xref="taxon:32630"
/noTe="chemically treated genomic
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/mol type="unassigned DNA"
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42.8%; Score 43.2; DE
Best Local Similarity 71.0%; Pred. No. 0.2;
Matches 71; Conservative 0; Mismatches
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Sequence 89 from Patent WO0200928.
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Sequence 19 from Patent W00200926.
AX344172
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1. .13249
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synthetic construct
artificial sequences.
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Unpublished
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TITLE
JOURNAL
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JOURNAL
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Rattus norvegicus clone CH230-134B20, WORKING DRAFT SEQUENCE.
AC098124
                                             4159 GGAATTTGGGGGTTAGGTTTTAGTCGGGGAAG-TCGTTTAGGAGCGCGCGAAATTTTT 4217
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Olek,A., Piepenbrock,C. and Berlin,K. Diagnosis of diseases associated with cell signalling Patent: WO 0202807-A 21 10-JAN-2002; Epigenomics AG (DE)
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HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="synthetic construct"
                                                                                                                                                                                                                                                                              AX348563 13249 bp
Sequence 21 from Patent WO0202807.
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AC098124/c
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DEFINITION
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VERSION
KEYWORDS
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SOURCE
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AX348563
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Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Gunzatne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, C., Hanilton, K., Harvey, Y., Havlak, P., Hames, A., Henderson, M., Hernandez, J., Haves, P., Haddm, S.L., Hodgson, A., Hogues, M., Hollins, B., Havells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, R., Jacob, L., Jacob, J., Kang, L., King, L., Johnson, R., Lui, Y., Liu, Y., Liu, Y., Lebow, H., Levan, J., Lewal, J., Lewal, J., Lewal, J., Lewal, J., Longare, S., Lopez, J., Liu, J., Liu, W., Liu, Y., Marth, R., Mandartne, M., Mahmodd, M., Malloy, K., Martinez, E., Song, Y., Scher, S., Socht, G., Shatsman, S., Strong, R., Wallson, E., Wal On May 10, 2003 this sequence version replaced gi:22855450.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.ed/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome table. Direct Submission Submitted (23-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, IX 77030, USA Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA Assembly program: Atlas 3.0; Consensus quality: 212229 bases at least Q40 Consensus quality: 213662 bases at least Q30 Web site: http://www.hgsc.bcm.tmc.edu/ Center: Baylor College of Medicine Center code: BCM Center clone name: CH230-134B20 Project Information Contact: hgsc-help@bcm.tmc.edu ----- Summary Statistics 3 (bases 1 to 228272)
Rat Genome Sequencing Consortium. Center project name: GGLR Genome Center (bases 1 to 228272) Direct Submission

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REFERENCE
AUTHORS
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Rattus norvegicus clone CH230-115H19, *** SEQUENCING IN PROGRESS
***, 3 unordered pieces.
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                                                                                                 NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces of believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
Consensus quality: 214533 bases at least Q20
Estimated insert size: 221650; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
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Rattus norvegicus (Norway rat)
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clone_end:Sp6"
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/note="wgs_end_extension
clone_end:Sp6"
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/note="wgs_end_extension
clone_end:Sp6"
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lone_end:Sp6
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TITLE JOURNAL

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AUTHORS

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Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davisland, C., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delagdo, O., Densen, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Digna-Rocha, S., Durn, A., Durbin, K., Dival, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Eranandez, S., Thiney, M., Flaggn, N., Porbes, L., Poster, M., Gebrer, P., France, C. M., Galbisi, A., Ganta, R., Garcia, A., Garrer, T., Garza, M., Gebregocygis, B., Geer, K., Gill, R., Grady, M., Guerra, M., Guevara, M., Harnandez, R., Hines, S., Hladun, S.L., Hadiun, C., Hamilton, K., Harnandez, R., Havlak, P., Hawes, A., Henderson, N., Hernandez, N., Havlak, P., Hawes, A., Henderson, N., Hernandez, M., Golvet, J., Jacoph, H., Ondeon, B., Johnson, R., Johnson, R., Johnson, R., Johnson, S., Jokkson, J., Lacob, L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Mcleod, M., Malloy, K., Manjur, R., Marine, P., Martine, S., Martinez, B., Mander, P., Martin, K., Martin, R., Martinez, B., Martinez, M., Malloy, R., Morris, S., Munidasa, M., Martinez, B., Martinez, M., Martinez, B., Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA.

Baylor Plaza, Houston, TX 77030, USA.

The sequence in this sequence version replaced gi:25007772.

The sequence in this assembly is a combination of BAC based reads and whole genome shortgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each consig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence Submitted (12-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature Center: Baylor College of Medicine Rat Genome Sequencing Consortium. Direct Submission (bases 1 to 258227) (bases 1 to 258227) Worley, K.C. Direct Submission

Center code: BCM Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu

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                                                                                                                                                                                                                                                                                                                     NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a "working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as Thus of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, C., Ayagi, A., Ayodeii, M., Bacas, E., Baden, H., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Cesar, H., Center, A., Chen, G., Cockrell, R., Cree, A., D'Souza, L., Cleveland, C., Cockrell, R., Coyle, M., Cree, A., D'Souza, L.,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                              Assembly program: Atlas 3.0;

Consensus quality: 217062 bases at least Q40

Consensus quality: 220975 bases at least Q30

Consensus quality: 223890 bases at least Q20

Estimated insert size: 227972; sum-of-contigs estimation

Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GGAACCTGGGGGTCAGGCCCCAGCGGGAAGCGCGCCCCAGGAGCGCGCGAAACCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 34.7%; Score 35; DB 2; Length 258227; 1 Similarity 61.5%; Pred. No. 21; 56; Conservative 0; Mismatches 35; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 255801: contig of 255801 bp in length
2 255901: gap of unknown length
2 25711: contig of 1210 bp in length
2 257211: gap of unknown length
2 258227: contig of 1016 bp in length.
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-115H19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 CCACACCCTTCCAGGCATTTGCCCGCCGCGA 91
                      Center project name: GKTX
Center clone name: CH230-115H19
------- Summary Statistics
Project Information
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/note="wgs_contig"
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AC130592.3 GI:24635281
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Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Davila, M.L., Davis, C., Ding, Y., Mangum, D., Mand, M., Martin, Y., Martin, Y., Mangum, D., Mand, Y., Martin, Y., Martin, Y., Mangum, D., Mangum, D., Martin, Y., Mand, Y., Martin, Y., Mangum, D., Mangum, D., Martin, Y., Mangum, D., Mangum,
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The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tun.ed/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
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Submitted (12-AUG-2002) Human Genome Sequencing Center, Department
Submitted (12-AUG-2002) Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 307042)
Rat Genome Sequencing Consortium.
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Center code: BCM Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu

Project Information

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musculus clone rp23-458j13 map 1 strain C57BL/6J, WORKING DRAFT
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1 (base 1 to 199471)

1i, J. Yang, L. and Roe, B.A.

Direct Submission

Direct Submission

Direct Submission

Direct Submission

Of Chemistry And Biochemistry,

The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,

OK 73019, USA
                                                                                                                                                    Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 199471)
Li,J., Yang,L. and Roe,B.A.
Mus musculus BAC Clone rp23-458jl3
                                                                                                                                                                                                                                                                                                                                          Li,J. Yang,L. and Roe,B.A. Direct Submission Submitted (24-AUG-2001) Department Of Chemistry And Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * NOTE: This is a "working draft' sequence. It currently consists of 8 contigs. Gaps between the contigs are prepresented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence as soon as it is available and the accession number will be preserved.

* This sequence as soon as it is available and is 39306 and a space of the preserved.

* This sequence as soon as it is available and the accession number will be preserved.

* 39305: contig of 39305 bp in length

* 39306 55773: contig of 16368 bp in length

* 72674 72673: gap of unknown length

* 72674 72673: gap of unknown length

* 72674 72773: gap of unknown length

* 179597 188934: contig of 86161 bp in length

* 179597 188163: gap of unknown length

* 179597 188163: contig of 86105 bp in length

* 188264 188263: gap of unknown length

* 188264 188263: gap of unknown length

* 188364 188263: gap of unknown length

* 188469 199471: contig of 8105 bp in length

* 106469 199471: contig of 8105 bp in length

* 106469 199471: contig of 8105 bp in length

* 106469 199471: contig of 8105 bp in length
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The University of Oklahoma
Center code:UOKNOR
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34.1%; Score 34.4; DE
Best Local Similarity 65.8%; Pred. No. 31;
Matches 50; Conservative 0; Mismatches
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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/clone_lib="RPCI - 2:
                              SEQUENCE, 8 ordered pieces. AC093452
AC093452.15 GI:38638756
HTG: HTGS PHASE2; HTGS DRAPT.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                               Unpublished
2 (bases 1 to 199471)
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                                                                                                                                                                                                                                                  * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* I 307042: contig of 307042 bp in length.
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il Similarity 61.5%; Pred. No. 21;
56; Conservative 0; Mismatcher 16. 76.
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/note="wgs_end_extension
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complement(6035..6875)
/note="clone_boundary
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/db_xref="taxon:10116"
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/note="clone_boundary
clone_end:Sp6
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                                                                                                                                                                                                                      AC093960 253540 bp DNA linear HTG 09-MAY-2003
Rattus norvegicus clone CH230-4G13, WORKING DRAFT SEQUENCE, 3
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
                                                                      52598 GCCGCGCACCCA 52583
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Worley, K.C.
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                  76 CATTTGCCCGCCGCGA 91
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Submitted (19-MXY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On May 9, 2003 this sequence version replaced gi:24818990. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.hom.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
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NOTE: This is a "working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
Direct Submission

Submitted (13-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

J (Dases 1 to 253540)

Rat Genome Sequencing Consortium.

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Assembly program: Atlas;
Consensus quality: 237398 bases at least Q40
consensus quality: 238410 bases at least Q20
Consensus quality: 238873 bases at least Q20
Estimated insert size: 246935; sum-of-contigs estimation
Quality coverage: 10x in Q20 bases; sum-of-contigs estimation
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5 245484: gap of unknown length
5 24668: contig of 1184 bp in length
9 246768: gap of unknown length
9 253540: contig of 6772 bp in length.
Location/Qualifiers
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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/clone="CH230-4613"
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Center clone name: CH230-4G13
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/note="wgs_contig"
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/note="wgs_contig"
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12. I (Dases I CO 25/344)

MADATIC., ADIATIC., Maltacker, M. Lee., Abramazon, S., Adams, C., Alder, J.,

Allen, C., Allen, H., Alsbrooks S., Amin, A., Anguianno, D.,

Allen, C., Allen, H., Alsbrooks S., Amin, A., Anguianno, D.,

Baddwin, D., Bandaramike, D., Barber, M., Barsstead, M., Benahmed, F.,

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Chacko, J., Chavez, D., Chen, C., Coyle, M., Cree, A., D' Souza, L.,

Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,

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Mangum, B., McLeod, M. P., Martin, R., Reitz, J., Start, S., Star
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.6, *** SEQUENCING IN PROGRESS
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                         9 GGGGTCAGGCCCCAGCCGCGGGAAGCGCCCCAGGAGCGCGCGAAACCTTCTCCACACCC
                                                    Gaps
                                                    0;
Length 253540;
Score 32.2; DB 2; Length 2
Pred. No. 1.2e+02;
0; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCII1855.4 GI:25006939
HTG; HTGS PHASE1; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                   120820 AGCACGACATAAACCCGCTGAGGTACAGCGAGC 120852
                                                                                                                                                                                                                   69 TICCAGGCATITGCCCGCCGCATICAGAGAGC 101
                                                                                                                                                                                                                                                                                                                                                                                  257344 bp DNR
Rattus norvegicus clone CH230-196H16,
***, 3 unordered pieces.
AC111855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 257344)
     31.9%;
59.1%;
                                                          55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus
                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus.
  Query Match
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AC111855/c
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                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
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Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Daylor Plaza, Houston, TX 77030, USA
ON Nov 15, 2002 this sequence version replaced gi:23270243.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.ugsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-seaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence conly contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 3 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                      Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (19-FEB-2002) Human Genome Sequencing Center, Departmen of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 257344) Rat Genome Sequencing Consortium.
Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 228515: contig of 228515 bp in length 228615: gap of unknown length le 256091: contig of 27476 bp in length 2 256191: gap of unknown length 2 257344: contig of 1153 bp in length. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Baylor College of Medicine
Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----- Project Information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---- Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .1227
/note="wgs_contig"
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LCFSVPQALLAARAGATYVSPFVGRVDDTGWDGSELIRQIKEAFVLGDIQTKVLAASI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="Aar1090r.1"
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PLPLALALLAGVLLPFVLRGLAAIPQAPALTLPTLIAYLLARVFARPRRAVPLALVTGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EAGRSYVNTIMNVYSFYULYANLDOPDIAAAPAVERPEMDRWLLARLEETVRDVTAA
LESYDARSGGRALEGFVDDLSNMYVRRSRSRFWGEGGTVDTAAYATLHEALLVVSQLT
APFTPFLADALYRNLSGEESSVHLTPWPTVRAERLDRKLTADMAAVMKVVELGRAVRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AHNIKTROPLAGVOYRAASPBALDAIKKSOTOIMEBINVKAVTFLEGDTDLVQYSLRP
NLPVVGKOYGKQLPVLKKALTBADARAVATAVQAGQGFSVQADGVTFDLTPGSVLVDA
KAPEGVAAAEDAGYLVAFDTALTPELVREGLARDLVRAIQEARKAAGFEVQDRIALAL
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AGTNPVKKEG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLGWLGRNHGASREELEEFNRLCRTSVWETIQDWNELTERMGYWLDLGDPYTTYQNSY
VESVWNLLRRLHEKGLVAQDYKVVPLSPRISSTLSRAELGEVDSYRMVDDPSVYVRLP
IVWDTLPERAHAALSSLSGEQRQGLSLLVWTTTPWTLPSNTLAAVNPDLDYVVADSPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GRVIVAAEGAVERLSALHKDAAPLEVLARFKGRDLEWVEYEPPFPEVASQLGVVSELHE
RRDGKPVLHFVVMADFVSDVDGSGVAHEAPAYGAEDLEVARAYGVPLMFGVDDHGILQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOVAGEMIAQNEKINWVPGNIKHGRFGNWLEGNVDWAISRERYWGTPLPFWQSESGQL
RVIGSVAELSELAGRDLSDLDLHRPYIDDITFTLDGEEYRRVPEVLDVWFDSGSMPYA
RSOPGIEAHMNVVLITLNLCRLEALRAAEGGGNLVFSLEDMKRRAYNALLAQVILSKL
DLSARFEELEHLPSSPLNFGLKAA"
                                                                                                                                                                                                                                           'note="similar to GB:X75439 GB:X59478 SP:P41368 PID:581558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="similar to GB:M76990 SP:P07775 PID:141751 percent identity: 59.18; identified by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="similar to GB:AE000657 percent identity: 74.31;
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                                                                                                                                                                complement(1432. .4668)
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                                                                                          complement (1432. .4668)
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                                                                                                                                                                                                                                                                                                                                     174799 GGGGACATGGCTCAGTTGGGGGAGGGCTGGCCTAGCGTGCGCCAAGCCATGGTCATCTCC 174740
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FRYGAGCHPAHLGSFWNGCAARTERGIEGSCCALIDVQHRQAFTVDVRGTRTGSBAPS
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VVIQQVGKKGQVTGYAVLFSTAVTMPAHEVIALYRSRFFIELIFRDAKQFLGGGDVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MNTPLPMGLMAILQYVLSAVPLRKTQRNFLTVLLSVFLAVPGRL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales; Deinococcacea, Deinococcus.

1 (bases 1 to 12557)

White,O., Eisen,J.A., Heidelberg,J.F., Hickey,E.K., Peterson,J.D., Dodson,R.J., Haft,D.H., Gwinn,M.L., Nelson,W.C., Richardson,D.L., Moffat,K.S., Qin,H., Jiang,L., Pamphile,W., Crosby,M., Shen,M., Wamathevan,J.J., Lam,P., McDonald,L., Utterback,T., Zalewski,C., Makarova,K.S., Aravind,L., Daly,M.J., Fraser,C.M. et al. Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1
                                                                                                                                                                                                                                                       68
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                                                                                                                                                                                                                                                   9 GGGGTCAGGCCCCAGCCGCGGGAAAGCGCCCCAAGAGCGCGCGAAACCTTCTCCACACCC
                                                                                                                                                                             Gaps
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Deinococcus radiodurans R1 section 117 of 229 of the complete
                                                                                                  Length 257344;
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/db_xref="G1:6459087"
                                                                                          Score 32.2; DB 2;
Pred. No. 1.2e+02;
0; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                        TICCAGGCATTIGCCCGCCGCGATTCAGAGAGC 101
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/chromosome="1"
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/gene="DR1334"
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/gene="DR1334"
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Deinococcus radiodurans R1
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/transT_table=1
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                                                                                                  31.9%;
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LOCUS
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/trānslation="msepdivpelavadlatsigewvnligfglkysrpebegfaylti
gnahsmldqiqqsrtwetaplqrplgrbinfeisvsdldvplarlmaadwplflapeb
kwyragdhetgvrqflvqDppGYLvrlsislgQCPLLQEATR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MNINDARDLITRLFTIIDSADYDRLGDVFAADAVYERPGYEPLO
GLPRIEGFYRHERVISGRHTVEDVTCSETGSAVSFGVFRGTSRAGEALEERPADVYR
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EPVWAIGTTADDABELAAAIRGALREQYGARAEGIRVLYGGSVKPENIAEICGK
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COMPLEMENT (9416. .9778)
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RPEEVTDPRESVQGAQVIASTFDEPPQHYRVAEFVHERARRIVEGGHVVILLDSIT
RLARANNIVTPPTGRTLGSGLDSNALHWRKRFIGAARNIREGGSLTILATALVETGRR
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                                        /note="similar to GB:L27276 PID:454814 SP:P52153 percent identity: 99.05; identified by sequence similarity; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="DR1340"
/note="similar to SP:P71604 PID:1552589 GB:AL123456
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/codon start=1
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complement (8620. .9354)
complement (8620. .9354)
/note="DR1339"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     producE="triosephosphate isomerase"
/protein_id="AAF10911.1"
/db_xref="GI:6459092"
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/transl_table=
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                         7198. .8478
/gene="DR1338"
gene="DR1338"
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31.7%; Score 32; DB 1; Length 12557;

Query Match

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5074 GGGGCCAGGGGTCAATGCGCCAATTCAGCGGAGGACCGCACGGAAGCGCGGGGGGGCGCTTT 5133
               ò
                                             Gaps
                 0;
 Pred. No. 1.7e+02;
0; Mismatches 40; Indels
                                                                                                                              5134 AGACAGCCCCCGGCCGCCGCCGCCGCCCAG 5169
                                                                                                        61 CCACACCCTTCCAGGCATTTGCCCCCCCGCGATTCAG 96
                                                                                                                                                                                7, 2004, 14:31:04
    58.3%;
                    56; Conservative
Best Local Similarity
Matches 56; Conserv
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Job time : 1059.25 secs
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CF181752 818731 MA

AA669625 nm38q05.s
BH14248 CAR1-HT014
CE26863 tigr-gsAQ373217 RPCT11-14
BX480547 DKPZP668C
BH057060 PM2-CN050
BH057060 PM2-CN050
AQ22280 AU122280
AQ385233 RPCT11-14
AA56430 PM2 FQH18
AA56644 EST7470-17
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AA551394 AR7110.s
AA631500 DRS 3400.x
AA605411 DRS 3400.x
AA605412 DRS 3400.x

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Eukaryota; Metazoa, Chordata, Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa, Chordata; Craniata; Ruminantia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.

Bovinae; Bovinae; Bos.

1 (Dases 1 to 832)

2 hao, S., Shetty, J., Shateman, S., Tsegaye, G., Geer, K., Crawford, A.M., Gebregeorgis, E., Chen, D., Riggs, F., de Jong, P., Crawford, A.M. and McEwan, J.C.

Bovine BAC End Sequences from Library CHORI-240

ND Unpublished (2003)

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the bovine BAC library CHORI-240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              632 bp DNA linear GSS 18-MAR-2003 GH240 195F24.TVB CHORI-240 Bos taurus genomic clone CH240 195F24, BZ850187
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BIX480547
BIX480547
BIX57060
AQ122280
AQ270807
AQ270807
AQ270807
AQ270807
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AQ2812
AQ664300
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AQ6912
AQ6013
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Bos taurus (cow)
Bos taurus
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46.4
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KEYWORDS
SOURCE
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CF362037 828421 MA
CE678956 tigr-gss-
CF364190 834119 MA
                                                                                                                                                                                               (without alignments)
1629.864 Million cell updates/sec
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                                                                                                                                                                       7, 2004, 13:34:53 ; Search time 1484.07 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55026578
                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                       27513289 seqs, 14931090276 residues
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Maximum Match 99%
Listing first 45 summaries
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CF362037
CE678956
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Gapop 10.0 , Gapext 1.0
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em_gss_mus:*
em_gss_pro:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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em_esthum:*
em_estin:*
em_estov:*
em_estpl:*
em_estro:*
em_htc:*
gb_estl:*
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14
129
14
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em_estom:*
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Match Length DB
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gb_est2:*
gb_htc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gb_est3:*
gb_est4:*
gb_est5:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gb_gss2:*
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4.48.6
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                                                                                                                                                                                                                                                                    Title:
Perfect score:
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CE414829 tigr-gss-BX492832 DKFZp781L CE603572 tigr-gss-BU688601 UI-CF-DUI

CE624617 tigr-gss-A1963674 wr64e08.x

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62

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Contact: Kirkness EF
The Institute for Genomic Research
Department of Enkaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                   165 AAGAAAGTGAGAAGACAACCCACAGAATGAGAAAAATATTTGCCAATCACATATCTGAT 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis. I (bases 1 to 652)
Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CE678956 tigr-gas-dog-17000313980922 Dog Library Canis familiaris genomic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TCAAGAAAGTGAAAACACACAGCAGCAGCAATAAAAATGTCTGTAAGTCATGTATCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 TCAAGAAAGTTAAAGAACCAACCCACAGAATCAGAAAAAATATTTGCAAATCATATTTA
                         /note="Wector: pcDNA3.1; Site 1: EcoR1; Site 2: Not1; Library made with RNA pooled from multiple tissues including brain, liver, muscle, placenta/endometrium, organ, testes and hone marrow "
                                                                                                                                                                                                                                                                     3 AAGAAAGTGAAAACACACACAGCAGAAGCAATAAAAATGTCTGTAAGTCATGTATCCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /.organism="Canis familiaris"
/mol type="genomic DNA"
/mol type="genomic DNA"
/mol type="genomic DNA"
/dolor="standard Poodle"
/dolorellb="Dog Library"
/note="Site 1: BetXI; Libraries were prepared from peripheral Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
                                                                                                                                                                     Query Match
60.0%; Score 48.6; DB 14; Length 603;
Best Local Similarity 75.9%; Pred. No. 0.0022;
Matches 60; Conservative 0; Mismatches 19; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 652;
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75.9%; Pred. No. 0.0022;
iive 0; Mismatches 19;
                                                                                             ovary, testes, and bone marrow.
     'clone lib="MARC 3PIG"
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Fax: 301-838-0208
Email: ekirknes@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genomic survey sequence.
CE678956
                                                                                                                                                                                                                                                                                                                                                                      63 TAGAGACTICTATCCAGGA 81
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Canis familiaris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Class: shotgun.
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Best Local Similarity
Matches 60; Conserv
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ORGANISM
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MEDLINE
PUBMED
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
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CE678956
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Plate: SRG8018 cow: J column: 16
Seq primer: GTAATACGACTCACTATAGGG.
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(http://www.chori.org/bacpac/bovine240.htm). For BAC library wardlability, please contact Pieter de Jong (pdejong@mail.cho.org) Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering_information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by AgResearch Ltd., New Zealand and The Institute of Genomic Research (TIGR), USA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 603)
2 Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Fox, J., Wise, T.A., Nonneman, D.J., Wray, J.E. and Keele, J.W.
A second set of porcine ESTs from a pooled-tissue normalized library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCAAGAAAGTGAAAACACACCCCCCGCAGAAGCAATAAAAATGTCTGTAAGTCATGTATCCG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 TCAAGAAAGTAAAAAGACAACCCACAAAATGAGGAAAAATATTTGCCAATCATGTATCTG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                     /_cell_type="Blood"
/clone_lib="CHORI-240"
/note="Vector: PTARBAC1.3; Site_1: Mbol; Site_2: Mbol;
Hereford bull in Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 50.6; DB 28; Length 832;
Pred. No. 0.00061;
0; Mismatches 19; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CF362037 603 bp mRNA linear
828421 MARC 3PIG Sus scrofa cDNA 5', mRNA sequence.
CF362037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TEL: 402 762 4390
                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/strain="breed: Hereford"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: smith@email.marc.usda.gov
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/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Sus scrofa"
                                                                                                                                                                                                                                                                                               /organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9913"
/clone="CH240_195F24"
                                                                                                                                                                       Plate: 195 row: F column: 24
Seg primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 62.5%;
1 Similarity 76.5%;
62; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sus scrofa (pig)
Sus scrofa
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Best Local S
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ACCESSION
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CF362037/c
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Email: cgapbs-remail.nih.gov.

Tissue Procurement: W. Mareton Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
DNA Sequencing by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/Link at:
www-bo.lnl.gov/bbrp/image/image.html
Insert Length: 339 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham.
PO Box 166, Clay Center, NE 68933-0166, USA rel: 402 762 4366 Fax: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross match v0.990329.
Plate: SRG8013 row: J column: 7 Seq primer: GTAATACGACTCACTATAGGG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA569625 109-SEP-1997 mRNA linear EST 09-SEP-1997 mm38905.sl NCI CGAP Pr4.1 Homo sapiens cDNA clone IMAGE:1062488 similar to contains L1.bl L1 repetitive element ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165 AAGAAAGTGAGAAGACAACCCACAGAATGAGAAAAAATATTTGCCAATCACATATCTGAT 106
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tissue_type="prostatic intraepithelial neoplasia - high/
                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="pooled"
/lab.bost="malous"
/lab.bost="malous"
/clome_lib="makc_3PIG"
/clome_lib="makc_3PIG"
/note="vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
Library made with RNA pooled from multiple tissues
including brain, liver; muscle, placenta/endometrium,
ovary, testes, and bone marrow."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 AAGAAAGTGAAAACACACACACAGAAGCAATAAAAATGTCTGTAAGTCATGTATCCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 701;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 60.0%; Score 48.6; DB 14; Best Local Similarity 75.9%; Pred. No. 0.0022; Matches 60; Conservative 0; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                       Location/Qualifiers
1. .701
/organism="Sus scrofa"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
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Homo sapiens
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Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
USDA, ARS, US Meat Animal Research Center
USDA 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4366
Fax: 402 762 4366
Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross match v0.990329.
Plate: SRG8020 row: P column: 19
Seq primer: GTAATACGACTCACTATAGGG.
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                                       EST 25-AUG-2003
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                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. (Dases I to 657)
Smith.T.P.L., Freking.B.A., Ford, J.J., Vallet, J.L., Fox, J., Wise, T.A., Nonneman, D.U., Wray, J.E. and Keele, J.W.
A second set of porcine ESTs from a pooled-tissue normalized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 AAGAAAGTGAAAACACCACAACCCGCAGAAGCAATAAAAATGTCTGTAAGTCATGTATCCGAT 62
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/db xref="taxon:9823"
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/tishue_type="pooled"
/clone_lib="WARC 3PIG"
/clone_lib="WARC 3PIG"
/note="Vector: pcDNA3.1, Site 1: BcoRI; Site 2: NotI;
/inche="type brain, liver, muscle, placenta/endometrium, ovary, testes, and bone marrow."
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1 (Dases 1 to 701)
Smith,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Fox,J.,
Wise,T.A., Nonnean,D.J., Wray,J.E. and Keele,J.W.
A second set of porcine ESTs from a pooled-tissue normalized
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.larity 75.9%; Pred. No. 0.0022;
Conservative 0; Mismatches 19; Indels 0;
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818731 MARC 3PIG Sus scrofa CDNA 5', mRNA sequence.
CF181752
                                     CF364190 657 bp mRNA linear 834119 MARC 3PIG Sus scrofa cDNA 5', mRNA sequence.
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USDA, ARS, US Meat Animal Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Sus scrofa"
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                                                                                                               CF364190.1 GI:34165561
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Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM1-HT0141-170 999-013-h05&t3=1999-09-17&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 12

High quality sequence stop: 361.
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1 (bases 1 to 36.)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Bordai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carralho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V. Simpson,D.H., Share,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
/clone libe "NCI CGAP Pr4.1"
//orte="Organ: prostate; Vector: pAMP10; mRNA made from prostatic intraepithelial neoplasia (high-grade), cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. cDNA Library Preparation: David B. Krizman, Ph.D. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE142248 361 bp mRNA linear EST 21-JUN-2000 CM1-HT0141-170999-013-h05 HT0141 Homo sapiens CDNA, mRNA sequence.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/dc_stage="Adult"
/clone lib="HT014"
/note="Organ: head_neck; Vector: pucl8; Site_1: Smal;
                                                                                                                                                                                                                                                                                                                                                                         1 TCAAGAAAGTGAAAACACAACCCGCAGAAGCAATAAAAATGTCTGTAAGTCATGTATCCG
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                                                                                                                                                                                                                                                                                  Score 47.4; DB 9; Length 360;
Pred. No. 0.005;
0; Mismatches 21; Indels
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The Institute for Genomic Research
Department of Entwaryciic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-388-0200
Fax: 301-338-0208
Bmail: ekirknes@tigr.org
Site 2: Smal, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                    0
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Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
                                                                                                                                                                                                                                                                                                  09
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tigr-gss-dog-17000359927985 Dog Library Canis familiaris genomic,
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/clone lib="bog Library"
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"
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The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
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                                                                                                                                                                                                     Length 361;
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                                                                                                                                                                                                     58.5%; Score 47.4; DB 10; 74.1%; Pred. No. 0.005; ive 0; Mismatches 21;
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/strain="Standard Poodle"
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CE268863
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Canis familiaris
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(bases 1 to 657)
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                    RPCTI1-146MZ0.TV RPCI-11 Homo sapiens genomic clone RPCI-11-146MZ0, sequence.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: hbe@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC

Library availability, please contact Pieter de Jong

(pieter@dejong med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

RACPAC Resources (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html

Seq primer: T?
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                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 643)
                                                                                                                                                                                                                                                                                                              Venter,J.C.

Wate of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
Unpublished (1997)
Other GSSs: RPCI11-146M20.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
PRI Institute for Genomic Research
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="Lymphocytes"
/clone lib="RPOT-11"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPOII1 Human Male BAC Library"
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                                                                                                                                                                                                                                                                                Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P.
Venter,J.C.
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/db_xref="GDB:7555987"
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/clone="RPCI-11-146M20"
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BX480547.1 GI:31917361
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AQ373217.1 GI:4344240
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                                                                                                                                                                                 Homo sapiens (human)
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BX480547/c
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 585) Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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PM2-GN0500-220201-002-h01 GN0500 Homo sapiens cDNA, mRNA sequence.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            \operatorname{Simpson}, A \cdot J \cdot Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                         This is the 5' sequence of the clone insert
This is the 5' sequence of the clone insert
Clone from 5. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKEZ); Email 8. Wiemann@dkfz- heidelberg.de,
sequenced by Qiagen (Hilden/Germany) Within the CDNA sequencing
consortium of the German Genome Project.
No s1 sequence available.
This clone (DKFZp686C23222) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin- Charlottenburg, GBRRMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hlcc3)"
Site_1: SfiIA; Site_2: SfiIB;
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Mewes, H.W., Weil, B., Amid, C., Osanger, A.,
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Bahr, A., Lauber, J., Mewes, H.W., Weil, B., Amid, Fobo, G., Han, M. and Wiemann, S.
EST (Eahr, A., Lauber, J., Mewes, H.W., Weil, B., Contact: MIPS
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Pred. No. 0.0046;
0; Mismatches 21;
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/note="Vector: pTriplEx2;
cDNA-collection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
mol_type="mRNA"
db_xref="taxon:9606"
/clone="DKFZp686C23222"
/dev stage="adult"
/lab_host="DH108"
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Fax: +55-11-2707001
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AU122280 Test 01-AUG-2002 AU122280 MAMMAI Homo sapiens cDNA clone MAMMAI002056 5', mRNA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 752)
                                                                                                                      /dev_stage="Adult"
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/note="Organ: placenta normal; Vector: puc18; Site_1:
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Bmail: genomicsehri.co.jp
Bmail: genomicsehri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAAGAAAGTGAAAACACAACCCGCAGAAGCAATAAAAATGTCTGTAAGTCATGTATCCGA
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 58.3%; Score 47.2; DB 12; Best Local Similarity 76.3%; Pred. No. 0.0053; Matches 58; Conservative 0; Mismatches 18;
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/clone lib="MAMMA1"
/note="Vector: pME18SFL3"
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/db_xref="taxon:9606"
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ocation/Qualifiers
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Contact: Takao Isogai
Genomics Laboratory
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1 (bases 1 to 625)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., Go'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
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  Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM2&t2=PM2-GN0500-
2202201-002-h01&t3=2001-02-22&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 523.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Pred. No. 0.0053;
0; Mismatches 18; Indels 0
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Email: asimpson@ludwig.org.br
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Fax: 301 838 0208
Fax: 301 838 0208
Edwal: bbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
library availability, contact Dieter de Jong
Dieterzdedjong.med.buffalo.edu, Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
Seq primer: SP6
Class: BAC ends.
                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Howo.

1 (bases 1 to 569)

1 Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter, J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Male"
/cell_type="Lymphocytes"
/clone_lib="RPCI-11"
/noce="Vector: pBAGe3.6; Site_1: EcoR1; Site_2: EcoR1;
RPCII1 Human Male BAC Library"
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                                                                                                                                                                                                                                             Unpublished (1997)
Other GSSs: RPCII1-141MI.TV
Other GSSs: RPCII1-141MI.TV
Contact: Shaying Thao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Fax: 301 838 0208
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73.8%; Pred. No. 0.008B;
iive 0; Mismatches 21
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/db_xref="GDB:7554048"
/db_xref="taxon:9606"
/clone="RPCI-11-141M1"
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  GI:4356256
                                             Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 462) Mahabaras, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
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462 bp DNA linear GSS 03-NOV-1998
HS 2059 A2 A07 MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2059 Col=14 Row=A, genomic survey
                                 21 TCAGGANAATGAAAAGACACCCCACAGAATGGGAAAAATTTTGTAAATCATATATCCG 80
  62
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/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
B-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
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    3 AAGAAAGTGAAAACACACCCCCCAGAAGCAATAAAAATGTCTGTAAGTCATGTATCCGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
High Throughput Saguencing Center
High Washington Center
401 Queen Anne Avenue North, Seattle, WA 98109, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=2059 Col=14 Row=A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2059 row: A column: 14
Class: BAC ends
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                                                                                                                                       680 AAGGGTCTAGTATCCAGAA 698
                                                                                            81
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                                                                                            63 TAGAGACTICTATCCAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
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Sequence 12549, A
Sequence 12549, A
Sequence 160, April
Sequence 48192, A
Sequence 48193, A
Sequence 48193, A
Sequence 48193, A
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                                                                                   7, 2004, 14:31:30 ; Search time 167.215 Seconds (without alignments) 2194.362 Million cell updates/sec
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1 tcaagaaagtgaaaacacaa......ttagagacttctatccagga
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11. | cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*

12. | cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*

13. | cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*

14. | cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*

15. | cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*

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18. | cgn2_6/ptodata/2/pubpna/USO0B.Sey:*

19. | cgn2_6/ptodata/2/pubpna/USO0B.Sey:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-311-455-89
US-10-085-783A-12549
US-10-242-535A-12549
US-10-082-192-160
US-10-087-192-160
US-10-027-632-48192
US-10-027-632-48194
US-10-027-632-48195
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US-10-027-632-48194
US-10-027-632-48195
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Maximum Match 99%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Sequence 78919, A Sequence 78919, A Sequence 78920, A Sequence 78921, A Sequence 314671,
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Sequence 41212, A
Sequence 202, App
Sequence 18323, A
Sequence 196, App
Sequence 196, App
Sequence 196, App
Sequence 18518, A
Sequence 6173, Ap
                                                                                                                    Sequence 314672,
Sequence 314673,
Sequence 314674,
Sequence 186, App
Sequence 187, App
Sequence 184, App
                           Sequence 78921, A Sequence 314671, Sequence 314672, Sequence 314673, Sequence 314673, Sequence 78918, A
                                                                                                                                                                             Sequence 76212,
Sequence 76212,
                    78920,
            Sequence
US-10-027-632-78918
US-10-027-632-78919
US-10-027-632-78920
US-10-027-632-314672
US-10-027-632-314672
US-10-027-632-314673
US-10-282-174-186
                                                                                                                                                                           13 US-10-027-632-76212
16 US-10-027-632-76212
9 US-09-920-455-146
                                                                                                                                                                                                      13 US-10-085-783A-41212
16 US-10-242-535A-41212
9 US-09-920-455-202
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US-09-814-353-6173
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9 US-09-920-455-196
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ALIGNMENTS

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RESULT 1

Sequence 90, Application US/10311455

Sequence 90, Application US/10311455

Publication No. US20030143606A1

GENERAL INFORMATION:

APPLICANT: PIERENBROCK, Christian

APPLICANT: BIELLANY: BIELLANY Kurt

TITLE OF INVENTION: Disquests of Diseases Associated with the Immune System by Deteir TITLE OF INVENTION: Disquests of Diseases Associated with the Immune System by Deteir TITLE OF INVENTION: Disquests PLING DATE: 2001-12-16

PRIOR APPLICATION NUMBER: PCT/PPO1/0737

PRIOR APPLICATION NUMBER: DE 10032529.7

PRIOR APPLICATION NUMBER: DE 10032529.7

PRIOR APPLICATION NUMBER: DE 1043826.1

PRIOR
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JULIA SEQUENCE 12549, Application US/10242535A

Publication No. US20040013663A1

GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: ChondroGene Inc.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
CURRENT APPLICATION NUMBER: US/10/242,535A

CURRENT FILING DATE: 2002-09-12

PRIOR APPLICATION NUMBER: US 60/305,783

PRIOR FILING DATE: 2001-07-28

PRIOR FILING DATE: 2001-07-28

PRIOR FILING DATE: 2001-03-12

PRIOR APPLICATION NUMBER: US 60/275,017

PRIOR APPLICATION NUMBER: US 60/275,017

PRIOR APPLICATION NUMBER: US 60/275,017

PRIOR APPLICATION NUMBER: US 60/271,955

PRIOR APPLICATION NUMBER: US 60/271,955
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APPLICANT: Engelhard, Eric
APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: A-71087/RMS/DCF
CURRENT APPLICATION NUMBER: US/10/052,482
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR PILING DATE: 2000-12-22
PRIOR PLIING DATE: 2001-03-02
                           Length 331;
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                        63.0%; Score 51; DB 13; Length 33 78.9%; Pred. No. 2.8e-07; ive 0; Mismatches 16; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (137)
; OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-12549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 TAAGGGACTTGTATCC 77
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Matches 60; Conservative
                                                                                     Conservative
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                           Query Match
Best Local Similarity
Matches 60; Conserv
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ORGANISM: Human
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US-10-052-482-58/c
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y Sequence 89, Application US/10311455
y Publication No. US20030143608A1
y Gequence 89, Application US/10311455
y Publication No. US20030143608A1
y GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
p APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Cytosine methylation
r TITLE OF INVENTION: Cytosine methylation
r TILE OF INVENTION: Cytosine methylation
r FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: DC7/EPO1/07537
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR PLING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
y WINDER OF SEQ ID NOS: 2424
SEQ ID NO 89
LENGHY: 13249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12549, Application US/10085783A;
Sequence 12549, Application US/10085783A;
Publication No. US20040037841A1
SEGNERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: ChondroGene Inc.
TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
FILE REFERENCE 4231/2002
CURRENT FFLING DATE: 2002-02-28
FRIOR APPLICATION NUMBER: US 60/305,340
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 12549
LENGTH: 331
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Pred. No. 2.7e-09;
0; Mismatches 14; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) NAME/KEY: misc_feature
) LOCATION: (137) .. (137)
; OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-12549
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ch 72.3%;
1 Similarity 82.7%;
67; Conservative (
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ORGANISM: Artificial Sequence
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Best Local Similarity
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                                 9481
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341 TCAAAAAAGTGAAAATACAACCAACAGAAAGAGAAAAAATATTTTCAAACCATGTATCTG 282
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Publication No. US20020198371A1

Publication No. US20020198371A1

GARDERAL PROFMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: POLYMorphisms in the Human Genome

TITLE OF INVENTION: POLYMorphisms in the Human Genome

TILE REFERENCE: 100827.129

CURRENT APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-09-20

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 1909-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR PRIOR PRILING DATE: 1999-09-08

PRIOR PRILING DATE: 1999-09-08

PRIOR PRILING DATE: 1999-09-08

PRIOR PRILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 125720

SOFTWARE PRESENCE OF Windows Version 4.0

SEQ ID NO 48193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58.5%; Score 47.4; DB 13; Length 74.1%; Pred. No. 5.6e-06; cive 0; Mismatches 21; Indels
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                                              FRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR PELING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1000-02-24
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
PRIOR PLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PRIOR FILING DATE: 1399-09-38
PRIOR FILING DATE: 1399-09-38
PRIOR PILING DATE: 1399-09-18
NUMBER OF SEQ ID NOS: 325720
SEQ ID NO 48192
LENGTH: 592
                                FILING DATE: 2000-07-12
APPLICATION NUMBER: US 60/198,676
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Best Local Similarity 74.1:
Matches 60; Conservative
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Best Local Similarity
Matches 60; Conserva
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US-10-027-632-48192
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REPERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                          NAME/KEY: misc_feature

| LOCATION: (70768)..(71491)

| OTHER INFORMATION: "n" at positions 70768 to 71491 can be any base

US-10-052-4812-58
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Publication No. US20020182586A1

GENERAL INFORMATION:
APPLICANT: MOTIS, David W.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: NOVEL CAMCER
FILE REFERENCE: 5.29452000122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-03-02

PRIOR FILING DATE: 2001-03-02

NUMBER OF SEQ ID NOS: 2059

SOFTWARE: FRESERE FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                      62.0%; Score 50.2; DB 12; 77.2%; Pred. No. 3.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60.5%; Score 49; DB 13; 75.3%; Pred. No. 9.3e-06; tive 0; Mismatches 20
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NUMBER OF SEQ ID NOS: 241
SOFTWARE: Patentin version 3.1
SEQ ID NO 58
LENGTH: 72332
                                                                                                                                                                                                                                                                                                                                                                                              61; Conservative
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                                                                                                              TYPE: DNA ORGANISM: Homo sapiens
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Best Local Similarity
Matches 61; Conserva
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US-10-027-632-48192/c
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LENGTH: 95683
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US-10-087-192-160
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Query Match
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341 TCAAAAAAAGTGAAAATACCAACCAACGAAAAGAGAAAAAAATATTTTCAAACCATGTATCTG 282
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US-10-027-632-48194/C

US-10-027-632-48194/C

Sequence 48194, Application US/10027632

Publication No. US20020198371A1

GENERAL INFORMATION:

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: POLYMORPHISE: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-12

PRIOR PELING DATE: 2000-04-20

PRIOR PELING DATE: 2000-03-29

PRIOR PELING DATE: 2000-02-24

PRIOR PELING DATE: 1999-11-23

PRIOR PELING DATE: 1999-11-23

PRIOR PELING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 48194

TAPP: NANA
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE REFERENCE: 108627.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2000-04.30
PRIOR APPLICATION NUMBER: US 60/128,676
PRIOR PILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-24
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10S-10-027-632-48195/c
i Sequence 48195, Application US/10027632
i Publication No. US20020198371A1
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                                                                                  61 ATTAGAGACTTCTATCCAGGA 81
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Best Local Similarity
Matches 60; Conserv
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US-10-027-632-48194
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Publication No. US20030204075A9

FRERRAL INFORMATION:
APPLICANTION:
APPLICANTION: Delymorphisms in the Human Genome
FILE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

FRIOR PLING DATE: 2000-07-12

FRIOR PLING DATE: 2000-07-12

FRIOR PLING DATE: 2000-07-20

FRIOR APPLICATION NUMBER: US 60/193,483

FRIOR PLING DATE: 2000-03-29

FRIOR PLING DATE: 2000-03-29

FRIOR FILING DATE: 1000-02-29

FRIOR PLING DATE: 1000-02-29

FRIOR PLING DATE: 1099-09-28

FRIOR APPLICATION NUMBER: US 60/156,358

FRIOR PLING DATE: 1999-09-28

FRIOR PLING DATE: 1999-09-28

FRIOR FILING DATE: 1999-09-08

FRIOR FILING DATE: 1999-08-09

FRIOR FILING DATE: 1999-08-09
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PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR PRILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 48195
LENGTH: 592
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                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Human
US-10-027-632-48195
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SEQ ID NO 48192
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0;

Gaps

; 0

Length 592; Indels 09

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341 TCAAAAAGTGAAAATACAACCAACAGAAAGAGAAAAAAATATTTCAAACCATGTATCTG 282
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                          58.5%; Score 47.4; DB 16;
74.1%; Pred. No. 5.6e-06;
ive 0; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THIER REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR PAPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-24
PRIOR PRIOR FILING DATE: 1999-12-3
PRIOR FILING DATE: 1999-12-3
PRIOR FILING DATE: 1999-10-3
PRIOR FILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-3
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-09-3
PRIOR FILING DATE: 1999-09-3
PRIOR FILING DATE: 1999-09-3
PRIOR FILING DATE: 1999-09-3
PRIOR PRIOR PRIOR DATE: 1999-09-3
PRIOR PRIOR PRIOR DATE: 1999-09-3
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR PRIOR FILING DATE: 1999-09-3
PRIOR PRIOR PRIOR DATE: 1999-09-3
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Publication No. US20030204075A9
GENERAL INFORMATION:
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Best Local Similarity
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; ORGANISM: Human
US-10-027-632-48195
                                                                  ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-48194
SEQ ID NO 48194
LENGTH: 592
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                                        Sequence 48193, Application US/10027632

Publication No. US2003204075A9

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

CURRENT APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR PRIOR TILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR APPLICATION NUMBER: US 60/146,002
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 10827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-24

PRIOR FILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-24

PRIOR PILING DATE: 2000-03-24

PRIOR FILING DATE: 2000-03-24

PRIOR FILING DATE: 2000-03-24

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-01-28

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-08-08

PRIOR FILING DATE: 1999-08-08

PRIOR FILING DATE: 1999-08-08

PRIOR FILING DATE: 1999-08-08

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-027-632-48194/c
Sequence 48194, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
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Matches 60; Conserv
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ORGANISM: Human
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                                                               1 TCAAGAAAGTGAAAACACACCGCAGAAGCAATAAAAATGTCTGTAAGTCATGTATCCG
                                   Gaps
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Query Match 58.5%; Score 47.4; DB 16; Length 592; Best Local Similarity 74.1%; Pred. No. 5.6e-06; Matches 60; Conservative 0; Mismatches 21; Indels 0
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Search completed: May 7, 2004, 17:35:53 Job time: 170.215 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Run on:

OM nucleic - nucleic search, using sw model

7, 2004, 13:35:03 ; Search time 40.6738 Seconds Мау

(without alignments)
1105.159 Million cell updates/sec

1 tcaagaaagtgaaaacacaa......ttagagacttctatccagga 81 US-10-071-411A-1_COPY_500_580 Title: Perfect score: Sequence:

Scoring table:

682709 segs, 277475446 residues IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Searched:

1365416

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0%
Maximum Match 99%
Listing first 45 summaries

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/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:* Issued Patents NA:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	1	Description	Seguence 59, App.	59,	59,	equence 59,	equence 59,	59	59,	Sequence 1342, Ap	H	m	27	N	3	'n	현	189,	Sequence 9585, Ap	3, A	Sequence 11, Appl	3, Ap	38	106,	11,	'n	10	'n	7
STANTED	Ę		US-09-040-984-59	US-09-123-912-59	S	ď	-615A-	10	US-09-221-107-59	US-09-016-434-1342	US-09-426-290-1	US-09-873-404-3	US-09-288-143-27	US-09-539-333D-211	US-09-816-095-3	-09-751-	-09-621-	-09-621-	-09-621-	-09-734-	-10-027-983-	-08-078-	US-09-621-976-3878	US-09-620-312D-106	US-10-027-983-11	US-09-852-067-3	US-09-791-211-10	US-09-818-512-3	US-08-991-789A-72
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Sequence 72, Appl	Sequence 72, Appl	Sequence 72, Appl	72,	1, A	30,	3, A	37,	Sequence 44, Appl	61,	185	184		7		3, An	191	-
US-09-062-451-72	US-09-598-326-72	US-09-289-198-72	US-09-429-755-72	US-09-783-203-1	US-09-733-294A-30	US-09-818-512-3	US-09-497-855A-37	US-09-497-855A-44	US-10-204-708-61	US-09-621-976-1855	US-09-621-976-1849	US-09-734-674-3	US-09-461-325-102	US-10-012-542-102	US-09-784-316-3	US-08-991-789A-191	US-09-062-451-191
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28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

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Sequence 59, Application US/09040984
; Patent No. 6210883
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
APPLICANT: Wang, TongTong
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS
; TITLE OF SEQUENCES: 86
; CORRESPONDENCES: 86
; CORRESPONDENCES: 86
; ADDRESSE: SEED and BERRY LLP
; STREET: Seatle
                                                                                                                                                                                                                                                                                                                                                       COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compartible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA.
APPLICATION DATA.
APPLICATION NUMBER: US/09/040,984
FILING DATE: 18-MAR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAXI, DAYIG.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.456
TELECOMMUNICATION INFORMATION:
TELEPHONE: 200-622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 649 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 206-282-6031
TELEX:
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COUNTRY: US
ZIP: 98104
JS-09-040-984-59/C
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US-09-040-984-59
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Gaps ; Length 649; Indels 22; Query Match

56.5%; Score 45.8; DB 3;
Best Local Similarity 72.8%; Pred. No. 1.6e-06;
Matches 59; Conservative 0; Mismatches 22;

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309 TCGATAAAGTGAAAACACAACACCACAGAATGGGAGAAAATTTTCCAAACCATGTATCTG 250 1 TCAAGAAAGTGAAAACACACCGCAGAAGCAATAAAAATGTCTGTAAGTCATGTATCCG 60 δ 셤

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APPLICANT:
APPLICANT:
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                                                                                                               Sequence 59, Application US/09123912A

Sequence 59, Application US/09123912A

Patent No. 6312695

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Wang, Tongtong

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER

FILE REPERENCE: 210121.455C1

CURRENT APPLICATION NUMBER: US/09/123,912A

PRIOR PILING DATE: 1998-03-18

NUMBER OF SEQ ID NOS: 114

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 59

LENGTH: 649
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56.5%; Score 45.8; DB 4; Length 649;

Best Local Similarity 72.8%; Pred. No. 1.6e-06;

Matches 59; Conservative 0; Mismatches 22; Indels (
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OTHER INFORMATION: Where n is a, NAME/KEY: modified_base
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LOCATION: (22)
OTHER INFORMATION: Where n is a,
NAME/KEY: modified_base
LOCATION: (190)
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OTHER INFORMATION: Where n is a,
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OTHER INFORMATION: Where n is a,
NAME/KEY: modified_base
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OTHER INFORMATION: Where n is a,
NAME/KEY: modified_base
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OTHER INFORMATION: Where n is a,
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61 ATTAGAGACTTCTATCCAGGA
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OTHER INFORMATION: Where n is NAME/KEY: modified base
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OTHER INFORMATION: Where n is NAME/KEY: modified_base
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                                                                                      RESULT 2
US-09-123-912-59/c
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                                                                                                                                                                                                                                                      APPLICANT: Li, Samuel X.

APPLICANT: Wannel X.

APPLICANT: Wang, Aijun
APPLICANT: Weekly, Yasir A.W.

APPLICANT: Henderson, Robert A.

APPLICANT: Henderson, Robert A.

APPLICANT: MCNeill, Patricia D.

ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGMOSIS OF LUNG CANCER

ITILE REPERBNCE: 210121.455C11

CURRENT APPLICATION NUMBER: US/09/643,597

CURRENT FILING DATE: 2000-08-21

NUMBER OF SEQ ID NOS: 369

SEQ ID NO 59

SEQ ID NO 59

LENGTH: 649
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APPLICANT: Fan, Liqun
APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REPERENCE: 210121.455C6
CURRENT APPLICATION NUMBER: US/09/480,884A
CURRENT APPLICATION NUMBER: US/09/480,884A
NUMBER OF SEQ ID NOS: 330
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH 649
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'Sequence 59, Application US/09480884A

'Patent No. 6482591;

'GENERAL INFORMATION:
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US-09-643-597-59/c
; Sequence 59, Application US/09643597
; Patent No. 6426072
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PARANISM: Homo sapien
FEATURE:
NAME/KEY: wisc_feature
LOCATION: INPORMATION: n = A,T,C or G
US-09-480-884A-59
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; LOCATION: (1)...(649)
; CTHER INFORMATION: n = A,T,C or G
US-09-643-597-59
                                                                                                                                                    Kalos, Michael D.
Bangur, Chaitanya S.
Hosken, Nancy
                                                                                                                                                                                                                                Fanger, Gary R.
Li, Samuel X.
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Matches 59; Conservative
                                                                         GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
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ORGANISM: Homo sapien
FEATURE:
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309 TCGATAAAAGTGAAAAACACAAAACGCAGAATGGGAGAAAAATATTGCAAAACCATGTATCTG 250
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TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER
FILE REFERENCE: 210121.45522
CURRENT APPLICATION NUMBER: US/09/221,107
CURRENT FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 161
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 59
LENGTH: 649
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NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 59
LENGTH: 649
TYPE: DNA
ORGANISM: Homo sapien
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CCATION: (1)...(649)

OTHER INFORMATION: n = A,T,C or G

US-09-606-421B-59
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NAME/KEY: modified_base
LOCATION: (433)
OTHER INFORMATION: Where n is a,
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LOCATION: (190)
OTHER INFORMATION: Where
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OTHER INFORMATION: Where
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OTHER INFORMATION: Where
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NAME/KEY: modified_base
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NAME/KEY: modified_base
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LOCATION: (550)
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Matches 59; Conserva
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                                                                                                                             FEATURE:
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  ch 56.5%; Score 45.8; DB 4; Length 649; l Similarity 72.8%; Pred. No. 1.6e-06; 59; Conservative 0; Mismatches 22; Indels
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APPLICANT: Skalky, Zasir A.W.
APPLICANT: Skalky, Zasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION UNMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
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APPLICANT: Ralos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REPERBUCE: 210121.455C8
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSEQ for Windows Version 3.0
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US-09-606-421B-59/c
; Sequence 59, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
                                                                                                                                                                                                                                                                                           US-09-542-615A-59/c
; Sequence 59, Application US/09542615A
; Patent No. 6518256
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; LOCATION: (1)...(649)
; OTHER INFORMATION: n = A,T,C or G
US-09-542-615A-59

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Bangur, Chaitanya S.
Hosken, Nancy
Fanger, Gary R.
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Best Local Similarity 72.8°
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                             Wang, Tongtong
Fan, Liqun
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ORGANISM: Homo sapien
    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Wang, T
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LENGTH: 649
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APPLICANT:
APPLICANT:
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APPLICANT:
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12256 TCAAGAGTATGAAAAGGAAAACCTACAAAATAGGAGAACATGTTTGGAAATCATGTATTTG 12315
                                                                                                                                                               ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
THEREOF
                                                                                                                       1 TCAAGAAAGTGAAAACACACACAGAAGCAATAAAAATGTCTGTAAGTCATGTATCCG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TCAAGAAAGTGAAAACACAACCCGCAGAAGCAATAAAAATGTCTGTAAGTCATGTATCCG
                                                                                  Gaps
                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 168575;
                                     52.6%; Score 42.6; DB 4; Length 4080; 70.4%; Pred. No. 2.9e-05; ive 0; Mismatches 24; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , 011;
hes 28; Indels
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    44.7%; Score 36.2; Di
1 Similarity 65.4%; Pred. No. 0.01.
53; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Berglind Ran Olafsdottir
APPLICANT: Jeffrey Gulcher
TITLE OF INVENTION: HUMAN NARCOLEPSY GENE
FILE REFERENCE: 2345.2001-000
CURRENT APPLICATION NUMBER: US/09/426,290
CURRENT FILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 168575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/873,404
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                                                                                                                                                                                                                                             3223 ATAAGGGCTTGTATCTGGAA 3243
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Patent No. 650066
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN KI
TITLE OF INVENTION: ACID MOLECULES F
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                           US-09-426-290-1
; Sequence 1, Application US/09426290
; Patent No. 6410712
; GENERAL INFORMATION:
                                                                                                                                                                                                       61 ATTAGAGACTTCTATCCAGGA
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                                     Query Match
Best Local Similarity 70.4;
Matches 57; Conservative
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ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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  US-09-016-434-1342
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US-09-426-290-1
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NAME/KEY:
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NAME/KEY:
LOCATION:
NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                       309 TCGATAAAGTGAAAACACAAACACCACAGAATGGGAGAAAATATTTGCAAACCATGTATCTG 250
                                                                                                                                                                                                                                                                                                                                                                 1 TCAAGAAAGTGAAACACAACCCGCAGAAGCAATAAAATGTCTGTAAGTCATGTATCCG 60
                                                                                                                                                                                                                                                                                                                           Gaps
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Patent No. 6500938

GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: PATHAX GENE EXPRESSION
TITLE OF INVENTION: PATHAX GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                   Length 649;
                                                                                                                                                                                                                                                                                                                           22; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                 Score 45.8; DB 4;
Pred. No. 1.6e-06;
0; Mismatches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTICATION NOWIDER:
ATTICATION TO THE CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: 9A-0002 US
TELEPANTUNICATION INFORMATION:
TELEPANTUNICATION 18F0-0555
INFORMATION FOR SEQ ID NO: 1342:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                 LOCATION: (594)
; OTHER INFORMATION: Where n is a, US-09-221-107-59
                                     LOCATION: (577) —
OTHER INFORMATION: Where n is a,
FEATURE:
                                                                                                                 LOCATION: (583) — OTHER INFORMATION: Where n is a,
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1 Similarity 72.8%;
59; Conservative
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FEATURE:
NAME/KEY: modified_base
                                                                                                NAME/KEY: modified base
                                                                                                                                                                                NAME/KEY: modified base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y: GENBANK
g34764
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Best Local Similarity
Matches 59; Conserva
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US-09-016-434-1342
                                                                                                                                                             FEATURE:
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Sequence 211, Application US/09539333D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55300 TCAACAGAGTAAATAGACAACCTACAGAATAGAAGAAAATATTTGCAAACTATGCATCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 AGAGTGAAAAGGTAACCTACAGAATGGGAGAAAATATTTGCAAACCATGTATCTAATAAG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TCAAGAAAGTGAAAACACACACAGCAACAATAAAAATGTCTGTAAGTCATGTATCCG 60
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                                                                                                                                                                                                                                                                                                                                                                                       Query Match 44.2%; Score 35.8; DB 4; Length 63588; Best Local Similarity 65.8%; Pred. No. 0.011; Matches 52; Conservative 0; Mismatches 27; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 44.0%; Score 35.6; DB 4; Length 788; I Similarity 67.6%; Pred. No. 0.0045; 50; Conservative 0; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Brewer et al.
TITLE OF INVENTION: 53 Human Secreted Proteins
FILE REFERENCE: PZ018P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 1999-04-08
CURRENT FILING DATE: 1999-04-08
CURRENT FILING DATE: 1999-04-08
EARLIER APPLICATION NUMBER: CT/US98/21142
EARLIER FILING DATE: 1999-10-08
EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/061,529
EARLIER APPLICATION NUMBER: 60/061,536
EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/061,536
EARLIER FILING DATE: 1997-10-09
CURRENT FILING DATE: 2001-06-05
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 63588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55240 ACAAAGGICTAATATCCAG 55222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-288-143-27/c sequence 27, Application US/09288143 patent No. 6433139 general INFORMATION:
                                                                                                                                                                                                                            NAME/KEY: misc_feature; ICCATION: (1)...(63588); OTHER INFORMATION: n = A,T,C or GUS-09-873-404-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ATTAGAGACTICTATCCAG 79
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 50; Conserva'
                                                                                                                                                    TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 27
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RESULT 12 US-09-539-333D-211

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Sequence 211, Application US/0953933D

Sequent No. 6476208

GENERAL INFORMATION:

APPLICANT: Cohen. Daniel

APPLICANT: Cohen. Daniel

APPLICANT: Cohen. Cohen.

APPLICANT: Blumenfeld, Marta

APPLICANTON WINDER: US (0)/130, 330

PRIOR APPLICANTON WINDER: US (0)/120, 903

PRIOR PLING DATE: 1999-03-30

PRIOR FILING DATE: 1999-04-30

PRIOR FILING DATE: 1999-07-14

PRIOR FILING DATE: 1999-07-14

PRIOR FILING DATE: 1999-07-14

PRIOR FILING DATE: 1999-07-29

PRIOR FILING DATE: 1999-10-28

PRIOR FILING DATE: 1999-10-12

NUMBER OF SEQ ID NOS: 231

LEAVENTE: LEAGURE DATE: 1999-10-12

NUMBER OF SEQ ID NOS: 231

LEAVENTE: LEAGURE DATE: 1999-10-12

PRIOR FILING DATE: 1999-10-12
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43.0%; Score 34.8; DB 4; Length 3001;
Best Local Similarity 65.4%; Pred. No. 0.012;
Matches 51; Conservative 0; Mismatches 27; Indels 0
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NAME/KRY: primer bind
LOCATION: 1905..1925
OTHER INFORMATION: downstream amplification primer, complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: 99-26781-25 : polymorphic base G or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: primer bind
LOCATION: 1477..1497
OTHER INFORMATION: upstream amplification primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc binding LOCATION: 1489-.1513
OTHER INFORMATION: 99-26781-25 probe
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LOCATION: 1502_.1521
OTHER INFORMATION: 99-26781-25.mis2,
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NAME/KEY: misc_binding
LOCATION: 1482..1500
OCHER INFORMATION: 99-26781-25.misl
FEATURE:
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LOCATION: 21,274..275
OTHER INFORMATION: n=a, g, c or t
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ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 1501
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367146 TCAACAAAGTGAATAGACAACCCACTGAATGGGAGAAAATATTTGCAAACTACCTATCTG 367087
                                                                                61 ATTAGAGACTTCTATCCAGGA
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: May Job time: 43.6738 secs
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Sequence 1, Application US/09751389
Patent No. 6630334
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
CURRENT APPLICATION NUMBER: US/09/751,389
CURRENT PILING DATE: 2001-01-02
NUMBER OF SEQ ID NOS: 8
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                     APPLICANT: GAN, Weiniu
APPLICANT: GAN, Weiniu
TITLE OF INVENTION: 1SOLATED HUMAN ENZYME PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOOL147
CURRENT APPLICATION NUMBER: US/09/816,095
CURRENT APPLICATION NUMBER: 2001-03-26
NUMBER OF SEQ ID NOS: 5
SOFTWARR: FASELSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 99916
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            1313 TGAGCAAAGTAAGCAGACAAACCCACAGAGTGAGAAAAAATATTTGCAAACTATGTATCTG 1372
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42.7%; Score 34.6; DB 4; Length 786431;
Best Local Similarity 64.2%; Pred. No. 0.053;
Matches 52; Conservative 0; Mismatches 29; Indels 0;
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0
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Pred. No. 0.032;
0; Mismatches 29; Indels 0;
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COTHER INFORMATION: n = A,T,C or G
US-09-751-389-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature

) LOCATION: (1)...(99916)

; OTHER INFORMATION: n = A,T,C or G

US-09-816-095-3
                                                                                                         1373 ACAAAGGACTAATATCCA 1390
                                                                                                                                                                                                                               Sequence 3, Application US/09816095 Patent No. 6664084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 64.2%;
Matches 52; Conservative
                                                              ATTAGAGACTTCTATCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 3
LENGTH: 786431
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US-09-751-389-3/C
                                                                                                                                                                               RESULT 13
US-09-816-095-3
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41.7%; Score 33.8; DB 4; Length 523;
Best Local Similarity 61.7%; Pred. No. 0.016;
Matches 50; Conservative 2; Mismatches 29; Indels
                                                                                                                                                                                                                                          APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET: 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT APPLICATION NUMBER: US/09/621,976
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 1442
LENGTH: 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: CDS
NAME/KEY: CDS
LOCATION: 188..472
NAME/KEY: sig_peptide
LOCATION: 188..295
OTHER INPORMATION: Won Heijne matrix
OTHER INPORMATION: score 7.80000019073486
OTHER INPORMATION: seq_CFVLLFFLRWSLT/XC
NAME/KEY: misc_feature
367086 ACAAGGAATTGATACCCAGAA 367066
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                                                                                                        US-09-621-976-1442/c
; Sequence 1442, Application US/09621976
; Patent No. 6639063
                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
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OTHER INFORMATION: n=a, g, c or t
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May 7, 2004, 11:56:28 ; Search time 165.476 Seconds (without alignments) 2079.475 Million cell updates/sec
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Maximum Match 99%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	-	о <u>щ</u> ол	Chemic Human		Aak77731 Human imm Ade43582 Polymorph	Ade43581 Human IDE Ade43315 Human IDE	Aah04914 Human cDN Aah17530 Human cDN	Continuation (3 of Abk53951 Human hea	Abk54007 Human hea Abk54004 Human hea	Abk54001 Human hea	Human Human
SUMMARIES	ABL32117 ABK31177	ABL70132 ABL32116 ABK31176	ABL70131 ADA02552	ADB72290 AAK77730	AAK77731 ADE43582	ADE43581 ADE43315	AAH04914 AAH17530	ADE11169_2 ABK53951_	ABK54007 ABK54004	ABK54001	AAC65798 ABL49017
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ABQ92203 ADA28618 ADE53578 AAC60048 AAC33258 ADA24348 ADC20114 AC742745 AAC50113 AAC53613 AAC54006 ABK53613 ABK54006 ABK54006 ABK54006 ABK64001	ALIGNMENT 249 BP.	ated gene S se; cytosir anamic; cy antidia ic; antidia leye disease leye disease loid arthrit 37. 29. 26.	ent of chem seases asso Sequence I s a number he methylat and treatme s retinopat
5.55 6.49	andard; DNA; 13	(first entry) e system associated ne system disease; sclerotic; antianae tive; antianatio; antiarthritic; antiarthritic; antiarthritic; ind leukaemia, Alzhe atosis; rheumatoid atosis; rheumatoid s 2001WO-EP007537. ; 2000DE-01032529. ; 2000DE-01043826. GENOMICS AG. epenbrock C, Berli	comprising fr treatment of ID NO 90; 32g nvention prover re modified b n the diagnor diseases suc
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	r 1 [17/c ABL32117 St	ABL32117; 26-MAR-2002 (fir. Human immune syst. Human; immune syst. Human; immune syst. antiarteriosclero acute myelodi leu neurofibromatosis ds. Homo sapiens. W0200200928-A2. 03-JAN-2002, 2000 01-SEP-2000; 2000 01-SEP-2000; 2000 01-SEP-2000; 2000 01-SEP-2000; 2000 01-SEP-2000; 2000 01-SEP-2000; 2000	Wucleic acid diagnosis an methylation. Claim 1, SEQ The present genes which can be used including ey
ପ୍ରତ୍ତ୍ତ୍ତ ବ୍ରହ୍ମ ବର୍ଷ ବିଷ୍ଟ୍ୟ ସ	RESULABLISE ID	**************************************	88888888888888888888888888888888888888

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The present invention relates to chemically modified DNA sequences of signal transduction associated genes. The DNA sequences are chemically modified using a solution of bisulphite, hydrogen sulphite or disciplinte.

Maso disclosed are oligonucleotides and/or PNA oligomers for detecting the cytosine methylation state (CpG islands) of these genes, and a method for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with signal transduction. The genomic DNA can be obtained from cells or cellular components which contain DNA, e.g. cell insue biopsies, blood, sputum, stool, urine, cerebral-spinal fluid, issue embedded in paraffin such as tissue from eyes, intestine, kidney, brain, heart, prostate, lung, breast or liver, histologic object slides, and all their possible combinations. The sequences of the invention are useful for the diagnosis and therapy of diseases associated with signal transduction e.g. solid tumours and cancer. ABK31158-ABK311545 represent chemically pretreated genomic DNA sequences of different genes associated
                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9541 ТСААААААТААБААСАСААССССАААААСАТАТАААТАТСТАТАААТСАТАТАТССС 9482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; signal transduction associated gene; cytosine methylation state; CpG island; signal transduction associated disease; solid tumour; cancer; antitumour; cytostatic; mutant; ds.
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   macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
                                                                                                                                                                                                                                                                                                                                                                                                           1 TCAAGAAAGTGAAAACACCCGCAGAAGCAATAAAAATGTCTGTAAGTCATGTATCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal transduction associated gene modified complementary DNA #10.
                               leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                    Sequence 13249 BP; 3128 A; 273 C; 3397 G; 6451 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                          / Match 74.6%; Score 60.4; DB 6; Length 13249; Local Similarity 85.9%; Pred. No. 8.6e-10; les 67; Conservative 0; Mismatches 11: Indels no
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01-SEP-2000; 2000DE-01043826.
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                                                                                                                                                                                                                                                              Query Match
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The invention relates to a nucleic acid comprising a sequence of at least with cell signaling. The activity of the modified sequences of the invention may be described as cytostatic. The object of the invention is to provide the chemically modified DNA of genes associated with cell signalling, as well as objectnollectides and/or DNA-digomers for particularly suitable for the diagnosis and/or DNA-digomers for particularly suitable for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with cell signalling. The chemically modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as solid tumours and cancer. The sequences given in records ABL7011-ABL70626 represent chemically pre-treated genemic DNA's of genes associated with cell signalling. Note requence data for this patent is not represented in the printed sequence in sequence information supplied by the
                                                                                                                                                                                                                                  9482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytosine methylation; cell signalling disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signaling e.g. cancer, comprises chemically modified genomic sequences of genes associated with cell signaling.
             sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                                                                                                  9541 TCAAAAAAATAAAAACACGCGCAAAAACAATAAAAATATCTATAAATCATATATCG
                                                                                                                                                                                                1 TCAAGAAAGTGAAAACACACACCCGCAGAAGCAATAAAAATGTCTGTAAGTCATGTATCCG
sequences. Note: The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chemically treated cell signalling DNA sequence complementary to#11.
                                                                                                                                                            0;
                                                                                      Sequence 13249 BP; 3128 A; 273 C; 3397 G; 6451 T; 0 U; 0 Other
                                                                                                                        Length 13249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 22; 24pp + Sequence Listing; English.
with signal transduction, or their complementary
                                                                                                                          Score 60.4; DB 6;
Pred. No. 8.6e-10;
                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                   9481 ATTAAAACTTCTATCCA 9464
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                                                                                                                                                                                                                                                                                                                                                                                            ABL70132 standard; DNA; 13249
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                                                                                                                          74.68;
                                                                                                                                           85.9%;
                                                                                                                                                                                                                                                                     61 ATTAGAGACTTCTATCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                           Local Similarity 85.9 es 67; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (EPIG-) EPIGENOMICS AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tumour; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cell signalling;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
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WC200200926-A2
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                                                                                                                                                         23-APR-2002
                                                                                                                                                                                                                                                                                                            03-JAN-2002.
                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                    ABK31176;
         3709
                                                                                                                                                                                                                                                                                                                                                                                                               olek A,
                                                                                                  ABK31176
                                                                                       RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid rebuxaemia, Alzheimer's disease, Alzheijepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine
                                                                  9
                                                                                                                                                                                                                                                                                                antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AlDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                  1 TCAAGAAAGTGAAAACACACCGCAGAAGCAATAAAATGTCTGTAAGTCATGTATCCG
                                            Gaps
                                                                                                                                                                                                                                                                                      Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13249 BP; 3594 A; 273 C; 3130 G; 6252 T; 0 U; 0 Other;
Sequence 13249 BP; 3128 A; 273 C; 3397 G; 6451 T; 0 U; 0 Other;
                                           0;
                                            11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 89; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                              Human immune system associated gene SEQ ID NO: 89.
                     Score 60.4; DB 6;
Pred. No. 8.6e-10;
0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Berlin K;
                                                                                                                                                                                            ABL32116 standard; DNA; 13249 BP.
                                                                                                                                     9481 ATTAAAACTTCTATCCA 9464
                                                                                                               ATTAGAGACTICIATCCA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-JUL-2001; 2001WO-EP007537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JUN-2000; 2000DE-01032529.
01-SEP-2000; 2000DE-01043826.
                      74.6%;
85.9%;
                                                                                                                                                                                                                                          26-MAR-2002 (first entry)
                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-130909/17
                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                  WO200200928-A2.
                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                       03-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              methylation.
                                            67;
                                                                                                                                                                                                                    ABL32116;
                      Query Match
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                                              Matches
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Traagaaagrgaaaararaarrcgragaagraaraaaaargrrigraagrrahgrargrah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful for the diagnosis and therapy of diseases associated with signal transduction e.g. solid tumours and cancer. ABK31158-ABK31545 represent chemically pretreated genomic DNA sequences of different genes associated with signal transduction, or their complementary sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; signal transduction associated gene; cytosine methylation state; CpG island; signal transduction associated disease; solid tumour; cancer; antitumour; cytostatic; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic sequences of genes associated with signal transduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13249 BP; 3594 A; 273 C; 3130 G; 6252 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal transduction associated gene modified DNA #10.
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                                                                                                                                                                                         ATTAGAGATTTTTÄTTTÄGGÄ 3789
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                                                                                                      81
                                                                                                      61 ATTAGAGACTICTATCCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                   ABK31176 standard; DNA; 13249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUN-2001; 2001WO-EP007472
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01-SEP-2000; 2000DE-01043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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72.3%; Score 58.6; DB 6; Length 13249; 82.7%; Pred. No. 3.3e-09;

1 TCAAGAAAGTGAAAACACCACAGAAGCAATAAAAATGTCTGTAAGTCATGTATCCG

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14; Indels

0; Mismatches

67; Conservative

Best Local Similarity

Matches

3769 ATTAGAGATTTTTATTAGGA 3789

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ADA02552/c

RESULT 7

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The invention relates to a nucleic acid comprising a sequence of at least 18 bases of a segment of chemically pretreated DNA of genes associated the chemical signal sign. The activity of the modified sequences of the invention may be described as cytostatic. The object of the invention is to provide the chemically modified DNA of genes associated with cell signalling, as well as oligonucleotides and/or bNA-oligomers for detecting cytosine methylations, as well as a method which is particularly suitable for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with cell signalling. The chemically modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as solid tumours and cancer. The sequences given in records ABL70111-ABL70626 represent chemically pre-treated genomic DNA's of genes associated with cell signalling. Note: The sequence data for this patent is not represented in the printed sequence data for this patent is not represented in the printed provided by the constitution supplied by the
                   3709 Traagaaagrgaaararaarrcgragaagraaraaaarrgrrigraagrrargrafitar
                                                                                                                                                                                                                                                                                                                                         Cell signalling; cytosine methylation; cell signalling disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signaling e.g. cancer, comprises chemically modified genomic sequences of genes associated with cell signaling.
Sequence 13249 BP; 3594 A; 273 C; 3130 G; 6252 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 21; 24pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                       Chemically treated cell signalling DNA sequence#11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 6;
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Pred. No. 3.3e-09;
                                                                                             3769 ATTAGAGATTTTTATTAGGA 3789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berlin K;
                                                           81
                                                                                                                                                                                         ABL70131 standard; DNA; 13249 BP
                                                           61 ATTAGAGACTTCTATCCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JUN-2000; 2000DE-01032529.
01-SEP-2000; 2000DE-01043826.
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82.7%;
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                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (EPIG-) EPIGENOMICS AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-154758/20.
                                                                                                                                                                                                                                                                                                                                                              tumour; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200202807-A2
                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified.
                                                                                                                                                                                                                                                                   01-JUL-2002
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                                                                                                                                                       RESULT 6
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The invention relates to recombinant carcinoma associated (CA) nucleic acid sequences from mouse and human (ADA01482-ADA03094), and to acid sequences from mouse and human (ADA01482-ADA03094), and to caccombinant carcinoma associated proteins (CAP) encoded by them. The invention also encompasses expression vectors and host cells comprising a character of the protein, and a blochip comprising CA nucleic acid or CA nucleic acid, a polypeptide (especially an antibody) that specifically concogenic retroviruses, which insert into the genome of the host organism at random. Many of these do not carry transduced host oncogenes or pathogenic trans-acting viral genes, meaning that cancer incidence is a circumparance of the effects of proviral integration into host protonocogenes. The CA nucleic acids of proviral integration into host carcinoma (especially breast cancer, prostate cancer, lymphoma or carcinoma is propensity to carcinoma by determination of the sequence of the invention of CA gene expression in particular cissues. CA nucleic acids, proteins and antibodies are also useful as thermal sequence represents a specifically claimed human CA nucleic acid cancer is a specifically claimed human CA nucleic acid cancer is the complete sequence data for this cancer is a specification, but was obtained in a lorency of the printed specification, but was obtained in a lorency of the concept of the carcinoma cancer is the complete sequence of the inventual transmitted or the printed specification, but was obtained in all not form part of the printed specification, but was obtained cancer in the complete sequence of the inventual cancer is the complete sequence of the carcinome of the printed specification, but was obtained to the carcinome of the c
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                                                                                                                                                                                                    Human, carcinoma associated; oncogene; carcinoma; cancer; breast; prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 72332 BP; 16680 A; 18843 C; 19431 G; 16654 T; 0 U; 724 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant nucleic acid encoding carcinoma associated protein, useful for preparing compositions for treating carcinomas.
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                                                                                                                                                 Human WNT3A carcinoma associated gene, SEQ ID NO:1070.
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ADA02552 standard; DNA; 72332
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                                                                                                                                                                                                                                                                                                                                                           WO2003057146-A2.
                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                06-NOV-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Morris DW;
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                                                                                                                                                                                                                                                       gene; ds.
                                                   ADA02552;
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Gaps

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3709 TTÄÄGÄÄÄÄGIGAÄÄTÄTAATTCGTÄGÄÄGTÄÄTÄAAÄÄÄGTTTGTÄÄGTTÄTGTÄTTCG 3768

61 ATTAGAGACTICTATCCAGGA 81

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1 TCAAGAAAGTGAAAACACACACCGCAGAAGCAATAAAAATGTCTGTAAGTCATGTATCCG 60

0; Mismatches 14; Indels

Conservative

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Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                   cytostatic; gene therapy; vaccine; metastasis; ds
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200005-0225757P
200005-0225758P
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200005-0226681P
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2000US-0225213P.
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2000US-0180628P.
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2000US-0216647P
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14-AUG-2000;
14-AUG-2000;
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18-AUG-2000;
22-AUG-2000;
22-AUG-2000;
22-AUG-2000;
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08-SEP-2000;
12-SEP-2000;
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30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
                                          Homo sapiens.
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07-JUN-2000;
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                                                                                                                                                24-FEB-2000;
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TCAAGCAAGTGAAAAGACAACCCACAGAATGGGGGAAAATATTTGCAAGTCATGTATTGG 35956
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                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel recombinant nucleic acid comprising a nucleotide sequence selected from any of the 660 sequences fully defined in the specification. A polymucleotide of the invention has cytostatic activity, and may have a use in gene therapy, or in a vaccine. The recombinant nucleic acids and polypeptides are useful for treating carcinomas, e.g. lymphomas, anothers, neoplasm, adenocarcinoma, and sarcommas. The present sequence represents a human gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                   recombinant nucleic acid, useful for treating carcinomas, lymphomas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 72332 BP; 16680 A; 18843 C; 19431 G; 16654 T; 0 U; 724 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                     human, ds, cytostatic, gene therapy, vaccine; carcinoma; lymphomas; cancer; neoplasm; adenocarcinoma; sarcoma; gene.
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Pred. No. 2.5e.06;
0; Mismatches 18; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                              cancers, neoplasm, adenocarcinoma, or sarcomas
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35955 ATAAGGGACTTGTATGCAG 35937
                                                    ВР
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                                                    72332
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23-CCT-2001; 2001US-00004113.
08-NOV-2001; 2001US-0005482.
30-NOV-2001; 2001US-00997722.
20-DEC-2001; 2001US-00034650.
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                                     entry)
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25-SEP-2000; 2000US-0234997P.
25-SEP-2000; 2000US-0235499P.
26-SEP-2000; 2000US-0235494P.
27-SEP-2000; 2000US-0235834P.
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29-SEP-2000; 2000US-023636P.
29-SEP-2000; 2000US-023636P.
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08-NOV-2000; 2000US-024660P.
08-NOV-2000; 2000US-024661P.
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17-NOV-2000; 2000US-0249218P.
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2000US-0249297P.
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02-0CT-2000;
13-0CT-2000;
20-0CT-2000;
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) anno acid sequences given in AAM92170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polymucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or delactions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polymucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the concleic acids into a host cell and culturing the used to provent, adjagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 concers and cancer human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 crepresent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4021 rcaaaaaagrgaaaagacaacrcacagaaagggagaaaarrrrgcaaarcargrarcrg 3962
                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 32542; 3071pp + Sequence Listing; English.
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2000US-0180628P.
2000US-0184664P.
2000US-0186350P.
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11-DEC-2000; 2000US-0254097P.
05-JAN-2001; 2001US-0259678P.
                                                                                                             (HUMA-) HUMAN GENOME SCI INC
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17-MAR-2000; 2000US-0190076P.
19-MAY-2000; 2000US-019113P.
19-MAY-2000; 2000US-0209467P.
26-JUN-2000; 2000US-021486FP.
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11-JUL-2000; 2000US-0217487P.
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14-SEP-2000; 2000US-0233148P.
14-SEP-
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13-OCT-2000; 2000US-0239337P.
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17-NOV-2000; 2000US-024921P.
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human immune/hematopoietic antigen polypeptides, diagnosing and/or treating cancers and metastasis. Nucleic acids encoding useful for preventing,

Disclosure, SEQ ID NO 32543; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I)

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   proteins and polynuclectides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) or polynuclectides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynuclectides may be used to prevent, cancers and cancer metastases of haematopoietic-delived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK5950 and AAM82169 crepresent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               Neurodegenerative disease; uPA; SNCG; IDE; KNSL1; LIPA; TNFRSF6; Alzheimer's disease; neuroprotective; nootropic; gene therapy; Chromosome 10; gene; ds.
                                                                                                                                                        Sequence 16535 BP; 4440 A; 3253 C; 3307 G; 5535 T; 0 U; 0 Other;
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"There is a variation at this position"
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"There is a variation at this position"
                                                                                                                                                                           Score 47.4; DB 4; Length 16535;
Pred. No. 1.6e-05;
0; Mismatches 21; Indels 0;
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"There is a variation at this position"
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"There is a variation at this position"
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                                                                                                                                                                                                                                                                                                                                                                                               Polymorphic human IDE genomic sequence, SEQ ID 187.
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"There is ?
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                                                                                                                                                                                                                                                                                                                                    ADE43582 standard; DNA; 128034 BP
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"There
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                                                                                                                                                                            58.5%;
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                                                                                                                                                                                                   60; Conservative
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                                                                                                                                                                             Query Match
Best Local Similarity
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2001US-0336929P
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08-NOV-2001; 2
08-NOV-2001; 2
09-NOV-2001; 2
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                                              28-MAR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                               (GEHO)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                 The present invention relates to a method (M1) for determining a predisposition for or the occurrence of neurodegenerative disease in a subject. The method comprises detecting in a target nucleic acid obtained from the subject the presence or absence of an allelic variant of one or more polymorphic regions of one or more genes selected from uPA (Urokinase plasminogen activator), SNGG (gamma-synuclein), IDE (insulinlypase), and TNRRSF6 (Thmour Necrosis Factor Receptor-SF6), where the presence of at least one of the allelic variant of one or more polymorphic regions is indicative of a predisposition for or the occurrence of neurodegenerative disease. The genes are all located on chromosome 10. M1 is useful for determining a predisposition for or the occurrence of and for treating neurodegenerative disease, particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                   Determining a predisposition for or the occurrence of neurodegenerative disease, e.g. Alzheimer's disease by detecting in a target nucleic acid the presence or absence of an allelic variant of one or more polymorphic
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 128034 BP; 34726 A; 25977 C; 26400 G; 40799 T; 0 U; 132 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TCAAGAAAGTGAAAACACAACCCGCAGAAGCAATAAAAATGTCTGTAAGTCATGTATCCG
                                                                                            Bertram L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neurodegenerative disease; uPA; SNCG; IDB; KNSL1; LIPA; INFRSF6; Alzheimer's disease; neuroprotective; nootropic; gene therapy; Chromosome 10; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 47.4; DB 9; Length 128034; Pred. No. 2.2e-05; 0; Mismatches 21; Indels 0;
                                                                                            Tanzi RE,
                                                                                            Wang X, Ta
                                                                                                                                                                                                              Claim 9; Page 584-page 618; 848pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human IDE genomic sequence, SEQ ID 186.
                                                                                             Elliott KJ,
                                                                                                         Sampson AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18912 ATAAGGGACTTGTATAGAGAA 18892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-OCT-2001; 2001US-0339525P.
  08-NOV-2001; 2001US-0338010P.
09-NOV-2001; 2001US-033853P
04-DEC-2001; 2001US-037052P.
28-MAR-2002; 2002US-0368919P.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 58.5%;
Local Similarity 74.1%;
nes 60; Conservative
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                                                           (MEUR-) NEUROGENETICS INC. (GEHO ) GEN HOSPITAL CORP.
                                                                                            Velicelebi G,
Mullin KM,
                                                                                                                                                                                                                                                                                                                                                                                         Alzheimer's disease.
                                                                                                                               WPI; 2003-559131/52.
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                                                                                                         Saunders AJ,
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18972 rcaagaaagrgaaaagacaaaccraragaarggcaraaaararrrigraarcaraararcrg 18913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a method (M1) for determining a predisposition for or the occurrence of neurodegenerative disease in a subject. The method comprises detecting in a target nucleic acid obtained from the subject the presence or absence of an allelic variant of one or more polymorphic regions of one or more genes selected from UPA (Urokinase plasminogen activator), SNCG (gamma-synuclein), IDE (insulindegrading enzyme), KNBLI (Kinesin-like protein I), LIPA (lysosomal acid lypase), and INRESF6 (Tumour Necrosis Factor Receptor-SPG), where the presence of at least one of the allelic variant of one or more polymorphic regions is indicative of a predisposition for or the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09
                                                                                                                                                                                                                                                                                                                                                                                                                                               Determining a predisposition for or the occurrence of neurodegenerative disease, e.g. Alzheimer's disease by detecting in a target nucleic acid the presence or absence of an allelic variant of one or more polymorphic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 occurrence of neurodegenerative disease. The genes are all located on chromosome 10. MI is useful for determining a predisposition for or the occurrence of, and for treating neurodegenerative disease, particularly
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                                                                                                                                                                                                                                                                          Bertram L;
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Alzheimer's disease; neuroprotective; nootropic; gene therapy;
Chromosome 10; gene; ds.
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                                                                                                                                                                                                                                                                              Tanzi RE,
                                                                                                                                                                                                                                                                          Elliott KJ, Wang X, The Sampson AJ, Blacker DL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 22; Page 549-584; 848pp; English.
                                                                                                                                                                                                                                                                       Elliott KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATAAGGGACTTGTATAGAGAA 18892
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2001US-0338010P.
2001US-0338363P.
2001US-0337052P.
                                                                                                          2002US-0368919P
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                                                                                                                                                                           (NEUR-) NEUROGENETICS INC
                                                                                                                                                                                                                                                                              Becker KD, Velicelebi G,
Saunders AJ, Mullin KM,
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5602 full-

Yamamoto J;

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Saito K, Otsuki

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The present invention describes primer sets for synthesisting bould this.

[any an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polyuacleotide which comprises one of the 5602 mucleotide sequences defined in the specification, where the complementary strand of a polyuacleotide which comprises one of the 5602 mucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 mucleotides; or (b) a combination of a noligonucleotide comprising a sequence complementary to the complementary strand of a polyuacleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a complementary strand of a polyuacleotide which comprises a 1'-end sequence complementary to a complementary strand of a sequence is selected from those defined in the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in cypecification. The primer sets can be used in antisense therapy and in cypecification and/or diagnosis of the abnormality of the proteins encoded by the full-length cDMAs. The primers are also betaining of the full-length cDMAs assily without any specialised methods. AAH33612 for AAH33623 represent human amino acid sequences; and AAH33622 represent compleotides.

Coligonucleotides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; primer; detection; diagnosis; antisense therapy; ss.
                                                                                                                                                                                                                                          Primer sets for synthesizing polynucleotides, particularly the 5602 full length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes primer sets for synthesising 5602 full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 AAGAAAGTGAAAACACAAACCCGCAGAAGCAATAAAAATGTCTGTAAGTCATGTATCCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             620 AAAAAAGIGAAAATACAACCCATAGAAAGATAAAAAATATTTTCAAGCCATGTATCTGAT
                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 1749; 2537pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 752 BP; 289 A; 140 C; 137 G; 183 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 47; DB 4; Length 752;
Pred. No. 1.2e-05;
                                                                                                                                      Hayashi K, S
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                            Wakamatsu
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                                                                                                                                  sogai T, Nishikawa T,
Sugiyama T, Wakamatsı
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 TAGAGACTICTATCCAGGA 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH17530 standard; cDNA; 1794
27-AUG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MRY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
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Best Local Similarity 74.7%;
Matches 59; Conservative
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                                                                                                                                                            Ishii S,
                                                                                                                                         Ota T,
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                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a method (M1) for determining a predisposition for or the occurrence of neurodegenerative disease in a subject. The method comprises detecting in a target nucleic acid obtained from the subject the presence or abone or an allelic variant of one or more polymorphic regions of one or more genes selected from UPA (Urokinase plasminogen activator), SNGG (gamma-synuclein), IDE (insulindegrading enzyme), KNSII (Kinesin-like protein 1), LIPA (lysosomal acid lypase), and TNPRSF6 (Tumour Necrosis Factor Receptor-SF6), where the presence of at least one of the allelic variant of one or more polymorphic regions is indicative of a predisposition for or the occurrence of neurodegenerative disease. The genes are all located on chromosome 10. M1 is useful for determining a predisposition for or the occurrence of and for treating neurodegenerative disease, particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                    Determining a predisposition for or the occurrence of neurodegenerative disease, e.g. Alzheimer's disease by detecting in a target nucleic acid the presence or absence of an allelic variant of one or more polymorphic regions.
                                                                                                                                                                                                      Bertram L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TCAAGAAAGTGAAAACACAAAACCCGCAGAAGCAATAAAAATGTCTGTAAGTCATGTATCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 202100 BP; 60747 A; 41352 C; 41113 G; 58888 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.5%; Score 47.4; DB 9; Length 202100; 74.1%; Pred. No. 2.4e-05; ive 0; Mismatches 21; Indels 0;
                                                                                                                                                                                                      Tanzi RE,
                                                                                                                                                                                                    Velicelebi G, Elliott KJ, Wang X, T, Mullin KM, Sampson AJ, Blacker DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cDNA clone (5'-primer) SEQ ID NO:1749.
                                                                                                                                                                                                                                                                                                                                                                                                          Claim 9; Page 769-823; 848pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104783 ATAAGGGACTTGTATAGAGAA 104803
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25-OCT-2001; 2001US-0339525P.
08-NOV-2001; 2001US-0336929P.
08-NOV-2001; 2001US-0338010P.
09-NOV-2001; 2001US-0338353P.
28-MAR-2002; 2002US-0368919P.
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                                                                                                                                                                  GEHO ) GEN HOSPITAL CORP
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                                                                                                                                           (NEUR-) NEUROGENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alzheimer's disease.
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                                                                                                                                                                                                                         Saunders AJ,
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Gaps

Indels

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The present invention describes primer sets for synthesising 5602 full-

[1 ength cDNAs defined in the specification. Where a primer set comprises:

[2 [2 [3] an Oligo-dr primer and an oligonucleotide comprisentary to the

[3 [3] complementary strand of a polynucleotide which comprises one of the 5602

[3 [3] complementary strand of a polynucleotide which comprises one of the 5602

[4 [3] complementary strand of a polynucleotide which comprises a formal of a polynucleotide comprising a sequence complementary to the

[5 [5] complementary strand of a polynucleotide which comprises a 5'-end

[5 [5] complementary strand of a polynucleotide which complementary to a sequence and an oligonucleotide comprises a 3'-end sequence, where the

[5 [5] complementary strand of a polynucleotide on the sequence of polynucleotide which comprises at least 15 nucleotides and the comblementary to a polynucleotide which comprises at least 15 nucleotides and the combination of the 5'-end sequence 5'-end sequence 5'-end sequence 5'-end sequence 6's end sequence 6's end sequence 6's end sequence 6's particularly full-length cDNAs. The primers are also useful for the comprises and comprises are also useful for the full-length cDNAs. The primers allow obtaining of the full-length cDNAs and primers allow obtaining of the full-length cDNAs and sequences; AAH13632 to AAH13632 represent human amino acid sequences; and AAH13632 to AAH13632 represent complementary and an eused in the exemplification of the complementary and an eused in the exemplification of the complementary and an eused in the exemplification of the complementary and an eused in the exemplification of the complementary special and the complementary and and and sequences and AAH13632 to AAH13632 represent the complementary and and the complementary and and the complementary and sequences and the complementary and the complementary and the complementary and the complementary 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; SEQ ID NO 17007; 2537pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                Ota I, Isogai I, Nishikawa I,
Ishii S, Sugiyama I, Wakamatsu
                                                                                                                  29-JUL-1999; 99JP-00248036.
27-ANG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-NAXY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
                                                            28-JUL-2000; 2000EP-00116126.
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   07-FEB-2001
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Saito K, Yamamoto J; , Otsuki T;

hikawa T, Hayashi K, Sa Wakamatsu A, Nagai K,

0; Gaps Score 47; DB 4; Length 1794; Pred. No. 1.4e-05; Sequence 1794 BP; 665 A; 328 C; 368 G; 433 T; 0 U; 0 Other; 20; Indels 0; Mismatches 58.0%; 74.7%; 59; Conservative Query Match Best Local Similarity Matches 59; Conserva

3 AAGAAAGTGAAAACACACAGAAGCAATAAAATGTCTGTAAGTCATGTATCCGAT 62

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Search completed: May 7, 2004, 13:50:26 Job time: 168.476 secs

AQ349913 RPCIII-12 CC489556 CH240.322 CE520001 tigr-9ss-CE45229 tigr-9ss-AQ10626 H3 3070.A CE533552 tigr-9ss-BZ387096 EINCM29TF AQ486453 RPCII1-15 AQ887236 HS 5552.B AZ043603 RFCI 23-3 CC471346 CH240.294 AI239979 qh44d09.x BX098B59 BX098B59 BW765852 saa48h09. AW183073 xj66e05.x BE041580 hof512.x AW183073 xj66e05.x BE041580 hof512.x AW183073 xj66e05.x AW181607 AV881607 AV881607 tigr-9ss-CE299189 tigr-9ss-CC2001389 HSL 51_CO CB084591 hq18b10.0 CB084591 hq18b10.0 BHZ03848 SM1-44X7. CC767238 BYS12389 CC67631 RPCI-11-3 CC67631 RPCI-11-3

e.

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AQ164003

HS 2270 Bl E07 MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2270 Col=13 Row=J, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota, Metazoa, Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae, Homo.
I (bases 1 to 313)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence-tagged connectors: A sequence approach to mapping and
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
10449764
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
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AQ106326

AQ106326

AQ048782

AQ0887236

AQ087236

AQ087236

AQ1339979

BX099859

BX091607

AV861607

AV861607

AV861607

AV861607

AV861607

AV861607

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AQ164003.1 GI:3562198
sequence.
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CC535951 CH240_414
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                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC 11brary availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Seq primer: 713 row: M column: 13
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1 (bases 1 to 416)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Feller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.
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Homo sapiens
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                                                                                                                                                                                                                                       /clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
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HS 5137 A1 G07 SP6E RPCI-11 Human Male BAC Library Homo sapien
genomic clone Plate=713 Col=13 Row=M, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ACAAAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCA
                                                                                                                                                                                                                                                                                                                                                    Score 34; DB 28; Length 313;
Pred. No. 2.8;
0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xef="teaxon:9606"
/clone="Plate=713 Col=13 Row=M"
/sex="male"
                                                                                                                                                         /organism="Homo sapiens"
/mol_trype="genomic DNA"
/mol_trype="genomic DNA"
/db xref="taxon:9606"
/clone="plate=2270 Col=13 Row=J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Mahairas GG, Wallace JC, Hood L
Fax: (206) 616-3887
Email: jwallace@u washington.edu
Sequence Tagged Connector
Plate: 2270 row: J column: 13
Class: BAC ends
High quality sequence stop: 313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 416.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQ442281.1 GI:4553620
                                                                                                                                                                                                                                                                                                                                                          66.7%;
nilarity 80.0%;
Conservative 0
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Best Local Similarity
Matches 40; Conserv
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AQ442281/c
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KEYWORDS
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CC335951 815 bp DNA linear GSS 17-JUN-2003 CH240 414P12.T7 CHORI-240 Bos taurus genomic clone CH240_414P12, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Kirkness EF
The Institute for Genomic Research
Department of Enkaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
/note="Vector: pBACe3.6; Site_1: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
                                                                                                                                                                                                        6
                                                                                                                                                                                                                                                                                                                                                                                                      GSS 26-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                          123 bp DNA linear GSS 26-SEP-20. Jgr-gss-dog-17000337092175 Dog Library Canis familiaris genomic, CE266277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Canis familiaris (dog)
Canis familiaris
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
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                                                                                                                                                                                                        Gaps
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Rithness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K. Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="rexon:9615"
/clone lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ACAAAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAA 45
                                                                                                                                                                                                                                                                                            388 AAATAGATAAATTGGACTTAATTTTAAAAACGTTTGTGCCTCAAA 344
                                                                                                                                                                                                                                                    45
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80.0%; Pred. No. 26;
artive 0; Mismatches 9;
                                                                                                                                                             28;
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                                                                                                                                                           Score 30.6; DB
Pred. No. 28;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /moi_type="genomic DNA"
/strain="Standard Poodle"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ekirknes@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:31854239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CE266277.1 GI:35989516
                                                                                                                                                           Query Match 60.0%;
Best Local Similarity 80.0%;
Matches 36; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 301-838-0200
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSS.
Bos taurus (cow)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Class: shotgun.
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CC535951.1
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ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

EN 1 (bases 1 to 382)

RS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
Venter,J.C.

Use of EAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building
Unpublished (1997)

Other GSS: RFCII-120E14.TJ

Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomics Research
9712 Madical Center Dr., Rockville, MD 20850

Tel: 301 838 0208

Email: hbe@igr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pletereddejong.med.bhffalo.edu). Clones may be purchased from
RACPAC Resources (http://bocpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search.page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQ34У913
RPCII1-120B14.TV RPCI-11 Homo sapiens genomic clone RPCI-11-120E14, genomic survey sequence.
                                                                                                                                                                                   Email: mdadams@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genetics (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html

Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pBACe3.6; Site 1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44
                                                                                              9712 Medical Center Dr., Rockville, MD 20850,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 AAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.4%; Score 29.8; DB 28; 82.9%; Pred. No. 47; 1ive 0; Mismatches 7;
                                                                             The Institute for Genomic Research
                         Contact: Mark Adams
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="Male"
/cell_type="Lymphocytes"
/clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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/db_xref="GDB:7513121"
/db_xref="taxon:9606"
/clone="RPCI-11-35C18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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Other GSSs: RPCI11-35C18.TJ
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Class: BAC ends.
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Best Local Similarity
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AQ349913/c
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KEYWORDS
SOURCE
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  COMMENT
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1 (Dases I to 491)

4 (Dases I to 491)

5 (Golden, K., Rouniley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Venter, J.C.

Venter, J.C.

Use of BAC End Sequences for Sequence-Ready Map Building (1998)

Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADVA/U26 SS 14-APR-1999 RPCIII-35C18.TK RPCI-11 Homo sapiens genomic clone RPCI-11-35C18, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: rholt@bcgsc.ca
Email: rholt@bcgsc.ca
(Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
(Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
British Columbia Genome Sciences Centre, Canada.
Plate: 414 row: P column: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                      1 (bases 1 to 8);
1 (bases 1 to 8);
1 Holt,R., Stott,J., Yang,G., Barber,S., Smailus,D., Prabhu,A.-L.,
Holt,R., Cloutier,A., Lee,D., Girn,N., Olson,T., Mayo,M.,
Butterfield,Y., Kirkpatrick,R., Liu,J., Guin,R., Chan,A.,
Schein,J., Marra,M., de Jong,P., Keele,J.W. and Kappes,S.M.
Bovine BAC End Sequences from Library CHORL-240, PLATES 399 to 478
Contact: Rob Holt
                                                      Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos
                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cll type="Blood"
/clone lib="CHORL-240"
/note="Wetcor: PTARBAC1.3; Site 1: Mbo1; Site 2: Mbo1;
Hereford bull 11 Domino 99375; CHORL-240 Bovine BAC
library (Male) produced by Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 The British Columbia Cancer Agency Genome Science Centre 600 W. 10th Ave, Vancouver, British Columbia, Canada VSZ 4E6 Tel: 604-877-6085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  274 AAAAAACAGGATTTCATTAAAGTTAAAACTTTTGTACTTCAAAGAACAT 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 29; Length 815;
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Pred. No. 33;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Bos taurus"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9913"
/clone="CH240_414P12"
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A0047026.1 GI:3315953
GSS.
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Best Local Similarity 74.5%;
Matches 38; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . .815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                              Sequencing
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SOUTCE

FEATURES

RESULT 5 AQ047026/c

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DEFINITION

ACCESSION VERSION KEYWORDS

ORGANISM

SOURCE

REFERENCE AUTHORS

TITLE JOURNAL

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Gaps

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CE454299 479 bp DNA linear GSS 27-SEP-2003 tigr-gss-dog-17000319453122 Dog Library Canis familiaris genomic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Kirkness EF
The Institute for Genomic Research
Department of Enkaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Canis familiaris (dog)
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Canis familiaris (dog)

Canis familiaris

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,

Mammalia, Butheria, Carnivora, Fissipedia, Canidae, Canis.

I (Dases I to 642)

Kirkness, B.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,

Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                   642 bp DNA linear GSS 28-SEP-20 genomic, genomic, genomic survey sequence.
/note="Vector: pTARBAC1.3; Site 1: Mbo1; Site 2: Mbo1; Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Canis familiaris"
/mol type="genomic DNA"
/strain="Standard Poodle"
/db xref="teaxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BarXI; Libraries were prepared from peripheral blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and comparative analysis
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                                                                                                                                                            Length 809;
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                                                                                                                                                                                                                                                                          45
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                                                                                                                                                            29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56.5%; Score 28.8; DB 75.0%; Pred. No. 89; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The dog genome: survey sequencing an Science 301 (5641), 1898-1903 (2003)
                                                                                                                                                         56.9%; Score 29; DB 77.8%; Pred. No. 75; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ekirknes@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genomic survey sequence
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                                                                                                                                                                                                                      35; Conservative
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Best Local Similarity
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AUTHORS
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PUBMED
COMMENT
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CE520001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CH240 322D15.T7 CHORI-240 Bos taurus genomic clone CH240_322D15, CH240_322D15, CH240_322D15, CH240_32CD15, CH240_32CD15, CH240_ACCEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 809)
1 (bases 1 to
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                         /mol_type="genomic_DNA"
/db_xref="dDB-7545805"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="RPAD="Lymphocytes"
/cell_type="Lymphocytes"
/clone_lib="RPCI-11"
/note="Westor: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Fax: 604-877-6276
                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                 56.9%; Score 29; DB 28; Length 382; 77.8%; Pred. No. 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          347 AAATAGATAAATTGGACTTAATTTTAAAACGTGTGTGCCTCAAA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ACAAAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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/strain="breed: Hereford"
                                                       organism="Homo sapiens"
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/cell_type="Blood"
/clone_lib="CHORI-240"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Bos taurus"
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/clone="CH240_322D15"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.809
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Matches 35, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus
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CC489556/c
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COMMENT
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0

Gaps

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BZ387096 841 bp DNA linear GSS 30-APR-2003
BINCM29TF BI_10_12_KB Entamoeba invadens genomic clone EINCM29,
genomic survey sequence.
BZ387096.1 GI:30233424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Kirkness EF
The Institute for Genomic Research
Department of Bukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
TT: 301-838-0208
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                             GSS 28-SEP-2003
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Canis familiaris
Canis familiaris
Canis familiaris
Canis familiaris
Mawanlia; Metazoa; Chordata; Craniata; Vertebrata; Butheria;
Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 669)
Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                           CES93552 linear GSS 28-SEP-20 tigr-gss-dog-17000366522943 Dog Library Canis familiaris genomic,
                                                                         /clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9615"
/clone_lib="bog_Library"
/note="Site_l: BstXI; Libraries were prepared from
peripheral Blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ·;
                                                                                                                                                                                                                                              .
                                                                                                                                                                                               55.3%; Score 28.2; DB 28; Length 265; 80.5%; Pred. No. 1.5e+02; ive 0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 669;
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                                                                                                                                                                                                                                                                                                                   219 AAACCAGACTGAACTTAATGTTAAAAATTTTTGTGCTTCAA 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54.5%; Score 27.8; DB 29;
illarity 82.1%; Pred. No. 1.8e+02;
Conservative 0; Mismatches 7;
/mol type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3070 Col=8 Row=1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Canis familiaris"
/wol type="genomic DNA"
/strain="Standard Poodle"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ekirknes@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genomic survey sequence.
CE593552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CE593552.1 GI:36910333
                                                                     sex="male"
                                                                                                                                                                                                                                                33; Conservative
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Matches 32; Conserv
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1 (bases 1 to 265)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Halinas, G.G., Mahairas, G.G., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSS 28-AUG-1998
                                                                                                                                                                           Contact: Kirkness BF
Contact: Kirkness BF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQ106326
HS_3070_A2_E04_MR_CIT_Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3070 Col=8 Row=I, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                    1 (bases 1 to 479)
Kirkhess, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9615"
/clone_lib="Dog_Library"
/note="Site_l: BEXII, Libraries were prepared from
peripheral blood"
                                                                                                              The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
    Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3070 row: I column: 8
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 479;
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                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Canis familiaris"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="Standard Poodle"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                     Email: ekirknes@tigr.org
Class: shotgun.
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AQ106326.1 GI:3481682
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/cell_type="Lymphocytes'
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/clone="EINGM29"
/clone="Tib="EIII of 12 KB"
/clone="vector: pHGS2; Site 1: BstXI; Total genomic DNA was isolated from early log phase trophozoites of E. invadens isolated from plant DNA extraction kit. A shotgum medium-size plasmid library (average insert size of 10 - 12 kb) was generated by random mechanical shearing of E. invadens genomic DNA, repairing the ends of DNA fragments with T4 Polymerase, adding BstXI adaptors and ligating into the BstXI site of a pUC-derived vector pHOS2."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pan troglodytes DNA, clone: PTB-028L09.R, genomic survey sequence. AG048782
AG048782.1 GI:16585674
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
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Fuljyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Tocoki, Y., Maranabe, H. and Sakaki, Y.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fuliyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
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                                                                                                                                                                                                                                                                                                           Medical Center Drive, Rockville, MD 20850, USA
                                     Entamoeba invadens
Eukaryota: Entamoebidae; Entamoeba.

1 (Bases 1 to 841)
Wang,Z., Samuelson,J., Clark,C.G., Eichinger,D., Bellen,K., Hall,W., Anderson,I. and Loftus,B.
Gene discovery in the Entamoeba invadens genome
Mol. Biochem. Parasitol. 129 (1), 23-31 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invadens"
                                                                                                                                                                                                                                                                                                                                                                         Email: enta@tigr.org
DNA was provided by Daniel Eichinger
Seg primer: TF
                                                                                                                                                                                                                        Other GSSs: BINCM29TR
Contact: Brendan Loftus
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Entamoeba in
/mol_type="genomic DNA"
/strain="IP-1"
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Location/Qualifiers
                     Entamoeba invadens
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Fax: 301-838-0208
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700 bp DNA linear GSS 21-WAY-1999
RPCII-154D12.TV RPCI-11 Homo sapiens genomic clone RPCI-11-154D12,
AQ386453
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Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library BCI-11. For BAC
Clones are derived from the human BAC library availability, please context Pieter de Jong
(pieter@dejong.med.buffalo.edu.clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (linfo@resgen.com). BAC end search page:
Seq primer: T7
Seq primer: T7
Class: BAC ends.
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1 (bases 1 to 700)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Ventex,J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC
was generated during the R&D process and may have higher chance
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0
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/mol_type="genomic DNA"
/mol_type="taxon:9598"
/clone="PTB-028L09.R"
/sex="male"
/clone=lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 646;
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Other GSSs: RPCIII-154DI2.TJ
Other GSSs: RPCIII-154DI2.TJ
Cobtact: Shaying Zhao, William Nierman, Mark Adams
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Enkaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850
713 838 0208
Fax: 301 838 0208
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Pred. No. 2.3e+02;
0; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
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/db_xref="GDB:7558835"
/db_xref="taxon:9606"
/clone="RPCI-11-154D12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1. .700
                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                 Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
                                                                                                                                           Sequencing: M13Rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ386453.1 GI:4357476
                                                                                         clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch
1 Similarity 75.6%;
34; Conservative (
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Homo sapiens
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Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center
University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887

Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 9320 row: J column: 6
Seq priner: SP6
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
/note="Vector Bace3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases I to 449) Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                     AQ887236
HS 5552 B2 E03 SPGE RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=9320 Col=6 Row=J, genomic survey sequence.
                                                                                                                                                                                    .
0
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                    Gaps
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                                                                                                                               Length 700;
                                                                                                                                                                                                                                                                                   545 ATATAGATAAATTGGACTTCAATAAAATTACTTGTGTGCGGAAA 501
                                                                                                                                                                                                                                         45
                                                                                                                                  Query Match 53.7%; Score 27.4; DB 28; Length Best Local Similarity 75.6%; Pred. No. 2.3e+02; Matches 34; Conservative 0; Mismatches 11; Indels
                                                                                                                                                                                                                                         1 ACAAAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="plate=9320 Col=6 Row=J"
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High quality sequence stop: 449.
Location/Qualifiers
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GSS.
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                                                                                                                                                                                 34; Conservative
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COMMENT
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AQ887236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
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Gaps

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4 AAAAGAAATIGGACTTAAAGTTAAATACTTTGTGCTTCAA 44

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253 ATAACAGACTGAACTTAATGTTAAAAAATNTTGTGCTTCAA 293
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Search completed: May 7, 2004, 15:42:23 Job time : 943.083 secs

Sequence 235079

US-09-984-429-344 US-10-087-192-658 US-10-027-632-235079 US-10-1311-455-1414 US-10-240-455-62 US-10-292-798-1333 US-10-282-738-31332 US-10-282-535A-31332 US-10-242-535A-31332

45698 105219

Sequence 235079, Sequence 114, Ap Sequence 1193, Appl Sequence 31332, A Sequence 31332, A Sequence 31332, A Sequence 268, Appl Sequence 268, Appl Sequence 268, Appl Sequence 1079, Appl Sequence 36924, A Sequence 36924, A Sequence 309812, Sequence 309812, Sequence 309812, Sequence 309812, Sequence 3133, Appl Sequence 22541,

598 5864 5864 822900 347 1214 1285 1285

Run

US-09-764-847-268
US-09-764-847-268
US-10-092-154-268
US-10-031-455-1979
US-10-027-632-36924
US-10-027-632-36924
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US-10-027-632-309812
US-10-027-632-309812
US-10-027-632-32541
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US-10-081-051-75
US-10-081-051-75
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US-10-081-051-75

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(without alignments)
2194.362 Million cell updates/sec
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| cgn2 6/ptodata/2/pubpna/USO7 PUBCOMB.seq:*
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| cgn2 6/ptodata/2/pubpna/USO7 NEW PUB.seq:*
| cgn2 6/ptodata/2/pubpna/USO8 PUBCOMB.seq:*
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| cgn2 6/ptodata/2/pubpna/USO8 PUBCOMB.seq:*
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| cgn2 6/ptodata/2/pubpna/USO9 PUBCOMB.seq:*
| cgn2 6/ptodata/2/pubpna/USO9 PUBCOMB.seq:*
| cgn2 6/ptodata/2/pubpna/USO9 NEW PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 99%
Listing first 45 summaries
                                                                                                                                                                       nucleic search, using sw model
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No.
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Sequence 74, Appl Sequence 1111, Ap Sequence 7470, Ap Sequence 82, Appl

US-10-081-051-74 US-10-311-455-1111 US-09-764-891-7470 US-10-052-482-82

5678 22927 87878

ALIGNMENTS

Sequence 297,

Sequence 15,

US-09-933-767-15 US-10-004-860-15 US-10-023-282-15 US-09-974-300-297

561 561 726 948 1018 1018

Sequence 322541, Sequence 75, Appl Sequence 57, Appl Sequence 15, Appl Sequence 15, Appl

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Sequence 89, Application US/10311455
; Publication No. US2003014366A1
; GENERAL INFORMATION:
    APPLICANT: OLEK, Alexander
; APPLICANT: OLEK, Alexander
; APPLICANT: DEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Dagnosis of Diseases Associated with the Immune System by Dete:
; TITLE OF INVENTION: Oytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT PAPLICATION NUMBER: DC1/216
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR PILING DATE: 2000-06-30
; PRIOR FILING DATE: 2000-06-30
; PRIOR FILING DATE: 2000-06-30
; RIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 89
; LENGHIA: 13249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
US-10-311-455-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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Sequence 89, Appl Sequence 248.89, Sequence 2248.89, Sequence 2248.89, Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 33.83,

US-10-027-632-224858 US-10-027-632-224858 US-10-027-623-224858 US-09-960-870-7 US-09-960-888-7 US-10-251-688-7 US-10-251-688-7 US-10-252-20-1 US-10-027-633-33533 US-10-027-633-33533 US-10-027-633-103827 US-10-027-632-103827

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605 605 879 10809 10809 580073

US-10-311-455-89 US-10-311-455-90

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Sequence 323533, Sequence 103827 Sequence 103827 . 0

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WESULIT 4

US-10-027-632-224858

US-10-027-632-224858

Sequence 224868, Application US/10027632

Publication No. US20030204075A9

GENERAL INFORMATION: US20030204075A9

GENERAL INFORMATION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: DAVIG G.

FILE REFERENCE: 108827.129

CURRENT FILING DATE: 2002-04-30

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR PLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-10-23

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FSSESQ for Windows Version 4.0

SEQ ID NO 224868

LENGTH: AND
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                           Length 605;
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                                                                                                                                                                                    9 AAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT 51
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                                   DB 13;
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                               58.4%; Score 29.8; Dilarity 79.1%; Pred. No. 12; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (1)...(605)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-224858
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Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
Query Match
Best Local Similarity
'-heq 34; Conservat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
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Matches
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                                           ## Application US/10311455

## Sequence 90, Application US/10311455

## Sequence 90, Application US/2030143606A1

### GENERAL INFORMATION:

### APPLICANT: OLEK, Alexander.

### APPLICANT: DLEK, Alexander.

### APPLICANT: DISGNOSSIS of Diseases Associated with the Immune System by Determ

### TITLE OF INVENTION: Gytcsine methylation

### TITLE OF INVENTION: Gytcsine methylation

### FILE REFERENCE: 5013.1014

### PRIOR FILING DATE: 2002-01-016

### PRIOR FILING DATE: 2000-06-30

### PRIOR FILING DATE: 2000-06-30

### PRIOR PRIOR PAPILCATION NUMBER: DE 10043826.1

### PRIOR PILING DATE: 2000-06-30

### RICH PILING DATE: 2000-06-30

### PRIOR PILING
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GENERAL INFORMATION:
GENERAL INFORMATION:
INFORMATION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILER REFERENCE: 10827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR PELING DATE: 2000-07-12
PRIOR PELING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 2000-08-20
PRIOR PELING DATE: 2000-02-20
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,218
PRIOR PELING DATE: 2000-02-24
PRIOR PELING DATE: 2000-02-24
PRIOR PELING DATE: 1999-103-28
PRIOR PELING DATE: 1999-103-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 75.3%; Score 38.4; DB 15; Length 13249; Local Similarity 87.5%; Pred. No. 0.059; es 42; Conservative 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 AAAAGAAATIGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | LOCATION: (1)...(605)
| OTHER INFORMATION: n = A,T,C or G
US-10-027-632-224858
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TYPE: DNA
ORGANISM: Artificial Sequence
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NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-027-632-224858
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                                              US-10-311-455-90/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 13249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-311-455-90
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Matches
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Best Local Similarity 72.5%;
Matches 37; Conservative
             Publication No. US20030138777A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 72.5
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: M. genitalium
US-09-960-858-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: M. genitalium
US-10-251-668-7
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US-10-251-668-7/c
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FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT APPLICATION NUMBER: 06/191,078

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-24

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-10-29

PRIOR PILING DATE: 2000-10-29

PRIOR PILING DATE: 2000-10-29

PRIOR PILING DATE: 2000-10-29

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-03-09

PRIOR PILIN
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Publication No. US20030134281A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICATION OF INVENTION:
TITLE OF INVENTION: USE
FILE REPERENCE: P.FA 4738
CURRENT APPLICATION NUMBER: US/09/960,870
CURRENT APPLICATION NUMBER: 2001-09-20
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 14; Indels
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Pred. No. 32;
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72.5%;
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Matches 37; Conservative
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US-09-960-870-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 37; Conserv
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US-10-282-122A-27417
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US-09-960-858-7/c
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Sequence 7, Application US/09960858

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Sequence 1, Application US/10205220

Beduence 1, Application WS/10205220

Bublication No. US20030170663A1

GRNERAL INFORMATION:

APPLICANT: Fraser et al.

TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma Genitalium Genome, Fragmer TITLE OF INVENTION: Thereof, and Uses Thereof

FILE REFRENCE : PAPPLICATION NUMBER: US/10/205,220

CURRENT APPLICATION NUMBER: US 08/545,528

PRIOR APPLICATION NUMBER: US 08/488,018

PRIOR PLING DATE: 1995-06-07

PRIOR PLING DATE: 1995-06-07

PRIOR PLING DATE: 1995-06-07

NUMBER OF SEQ ID NOS: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ACAAAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT 51
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APPLICANT: Evans, Glen; APPLICANT: Evans, Glen; TITLE OF INVENTION: USE; FILE REFERENCE: P.EA 5441; CURRENT ELLING DATE: 2002-09-20; PRIOR APPLICATION NUMBER: US 09/960,607; NUMBER OF SEQ ID NOS: 19; SOFTWARE: FastSEQ for Windows Version 4.0; FACUL NO 7; FACUL
GENERAL INFORMATION:
APPLICANT: Evans, Glen
TITLE OF INVENTION: USE
TITLE OF INVENTION: USE
FILE REFREENCE: P-EA 4974
CURRENT APPLICATION WUMBER: US/09/960,858
CURRENT FILING DATE: 2001-09-20
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PASLEGG for Windows Version 4.0
LENGTH: 10809
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Pred. No. 59;
0; Mismatches
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Pred. No. 59;
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Gaps
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Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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                                                                                                                                                                                                                                                                                                                 51.4%; Score 26.2; DB 13; Length 493; 72.3%; Pred. No. 1.5e+02; ive 0; Mismatches 13; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 CAAAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACAT 48
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TITLE OF INVENTION: Identification and Mapping of Sing
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 26.2; DB 16;
Pred. No. 1.5e+02;
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PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,006

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR PILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/195,218

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR PILING DATE: 2000-02-24

PRIOR PILING DATE: 1999-11-23

PRIOR PILING DATE: 1999-11-23

PRIOR PILING DATE: 1999-09-28

PRIOR PILING DATE: 1999-09-28

PRIOR PILING DATE: 1999-09-28

PRIOR PILING DATE: 1999-09-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: PASESEQ FOR WINDOWS VERSION 4.0

SOFTWARE: PASESEQ FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 32533
LENGTH: 493
TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 323533, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
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72.3%;
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Best Local Similarity 72.3
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 72.3
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-027-632-323533/c
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APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Rovalic David K
APPLICANT: Should A Company Should 
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Learning in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT PILING DATE: 2002-04-30
FRIOR REPLICATION NUMBER: US 60/218,006
FRIOR APPLICATION NUMBER: US 60/128,006
FRIOR PILING DATE: 2000-07-12
FRIOR APPLICATION NUMBER: US 60/199,676
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 2000-03-29
FRIOR PILING DATE: 2000-03-29
FRIOR PLING DATE: 2000-03-24
FRIOR PLING DATE: 2000-02-24
FRIOR APPLICATION NUMBER: US 60/167,363
FRIOR PILING DATE: 1999-10-23
FRIOR PILING DATE: 1999-10-23
FRIOR APPLICATION NUMBER: US 60/156,358
FRIOR APPLICATION NUMBER: US 60/156,358
FRIOR APPLICATION NUMBER: US 60/156,002
FRIOR APPLICATION NUMBER: US 60/156,002
FRIOR PILING DATE: 1999-09-09
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                                                                                                                                                                                                                                                                 Score 28.6; DB 15; Length 580073;
Pred. No. 1.6e+02;
0; Mismatches 14; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                 TCAAACATCAT 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49
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US-10-424-599-8350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 8350, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                        ; TYPE: DNA
; ORGANISM: Mycoplasma genitalium
US-10-205-220-1
        SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 72.5%;
Matches 37; Conservative
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US-10-027-632-323533/c
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US-10-424-599-8350
                                        SEQ ID NO 1
LENGTH: 580073
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| Sequence 103827, Application US/10027632
| Publication No. US2003024075A9
| GENERAL INFORMATION:
| APPLICANT: Wang, David G.
| TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
| TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
| TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
| TITLE OF INVENTION: Polymorphisms in the Human Genome
| TITLE OF INVENTION: Polymorphisms in the Human Genome
| TITLE OF INVENTION: VOUMBER: US/10/027,632
| CURRENT APPLICATION NUMBER: US 60/138,006
| PRIOR FILING DATE: 2000-04-20
| PRIOR FILING DATE: 2000-04-20
| PRIOR FILING DATE: 2000-04-20
| PRIOR FILING DATE: 2000-03-29
| PRIOR FILING DATE: 2000-03-29
| PRIOR APPLICATION NUMBER: US 60/165,363
| PRIOR FILING DATE: 1999-11-23
| PRIOR FILING DATE: 1999-10-24
| PRIOR FILING DATE: 1999-108-08
| PRIOR FILING DATE: 1999-09-28
| PRIOR FILING DATE: 1999-09-28
| PRIOR FILING DATE: 1999-09-28
| PRIOR FILING DATE: 1999-09-08-09
| PRIOR FILING DATE: 1999-08-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.4%; Score 26.2; DB 13; Length 1371; 72.3%; Pred. No. 1.9e+02; ive 0; Mismatches 13; Indels 0;
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PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
SEQ ID NO 103827
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 103827
LENGTH: 1371
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US-09-984-429-344
; Sequence 344, Application US/0998429
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Best Local Similarity 72.34
Matches 34; Conservative
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US-10-027-632-103827/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
, ORGANISM: Human
US-10-027-632-103827
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US-10-027-632-103827
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Sequence 5, Appli
Sequence 105, Appli
Sequence 1069, Appli
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Sequence 3, Appli
Sequence 1552, Appli
Sequence 1552, Appli
Sequence 1082, Appli
Sequence 10, Appli
Sequence 1, Appli
Sequence 173, Appli
Sequence 177, Appli
Sequence 177, Appli
Sequence 117, Appli
Sequence 117, Appli
Sequence 118, Appli
                                                                      7, 2004, 13:35:03 ; Search time 25.6094 Seconds (without alignments) 1105.159 Million cell updates/sec
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51
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1. / GgTZ_6/ptodata/2/ina/5A_COMB.seq:*

2. / CgTZ_6/ptodata/2/ina/5B_COMB.seq:*

3. / CgTZ_6/ptodata/2/ina/6A_COMB.seq:*

4. / CgTZ_6/ptodata/2/ina/6B_COMB.seq:*

5. / CgTZ_6/ptodata/2/ina/PcTTS_COMB.seq:*

5. / CgTZ_6/ptodata/2/ina/PcTTS_COMB.seq:*

6. / CGTZ_6/ptodata/2/ina/PcTTS_COMB.seq:*
GenCore version 5:1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-567-558-15

US-08-57-680A-3

US-08-475-891A-3

US-08-475-891A-3

US-09-976-594-1069

US-09-976-594-1069

US-09-976-594-886

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US-09-976-594-1069

US-09-976-594-1069

US-09-976-594-1078

US-09-134-001C-1128

US-09-596-002-10

US-09-596-002-10

US-08-956-171E-530

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US-09-9134-001C-1118

US-09-328-352-2188
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Maximum Match 99%
Listing first 45 summaries
                                                - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Match Length DB
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48.2 1018
47.8 3921
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                                                                                                                                                 Sequence:
                                                                                                                                                                                                              Searched:
                                                                         Run on:
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                                                                                                                        Title:
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29 22.4 43.9 36159 4 US-09-749-588-3 22.2 43.5 1281 4 US-09-134-001C-2724 31 22.2 43.5 1281 4 US-09-543-681A-3265 32 22.2 43.5 1628 4 US-09-580-729-29 33 22.2 43.5 1628 4 US-09-368-383C-6 34 22.2 43.5 1628 4 US-09-368-383C-6 34 22.2 43.5 1628 4 US-09-368-383C-17 35 22.2 43.5 3321 4 US-09-368-383C-17 38 22.2 43.5 5955 4 US-09-358-383C-17 38 22.2 43.5 5955 4 US-09-358-383C-17 39 22.2 43.5 5955 4 US-09-358-383C-17 4 US-09-368-383C-17 4 US-09-368-382C-18 4 US-09-368	Mycoplasma Genitalium Genome, Fragmer 4; Length 580073; 14: Indels 0; Gaps 0; 37GCTTCAAACATCAT 51 TCCTTTAACAGTAAT 508526
43.9 36159 4 43.5 813 4 43.5 1245 4 43.5 1281 4 43.5 1618 4 43.5 1626 4 43.5 2694 4 43.5 26001 4 43.5 5107 4 43.1 1044 4 43.1 1044 4 43.1 1044 4 43.1 1046 2 43.1 1046 2 43.1 1046 2 43.1 1047 2 43.1 1082 3 43.1 1782 3 43.1 1782 3 43.1 1982 0 60 00 00 00 00 00 00 00 00 00 00 00 00 0	
	ESULT 1 Sequence 1, Application US/08545528D Patent No. 653773 Sequence 1, Application US/08545528D Patent No. 653773 TITLE OF INVENTION: Nucleotide Sequence of tring FILE PRINCE PRIOR NUMBER: US/08/545,528D CURRENT APPLICATION NUMBER: US/08/545,528D CURRENT PILING DATE: 1995-10-19 PRIOR APPLICATION NUMBER: US 08/488,018 PRIOR FILING DATE: 1995-10-19 PRIOR PELICATION NUMBER: US 08/488,018 PRIOR FILING DATE: 1995-06-07 REIOR PELICATION NUMBER: US 08/488,018 PRIOR FILING DATE: 1995-06-07 REIOR PELICATION NUMBER: US 08/488,018 PRIOR FILING DATE: 1995-06-07 REIOR APPLICATION NUMBER: US 08/488,018 PRIOR FILING DATE: 1995-06-07 NUMBER OF SEQ ID NOS: 1 SOUTWARE: PatentIn version 3.1. ENGITH: 580073 TYPE: DNA ORGANISM: Mycoplasma genitalium SOUGANISM: Mycoplasma genitalium SOUGANISM: Mycoplasma genitalium SOUGANISM: Mycoplasma genitalium SOUGANISM: Wycoplasma
28 22.4 39 22.2 39 22.2 39 22.2 39 22.2 39 22.2 39 22.2 34 22.2 36 22.2 37 22.2 38 22.2 44 22.2 44 22.2 44 22.2 44 22.2 45 22.2 46 22.2 47 22.2 48 22.2 48 22.2 49 22.2 49 22.2 41 22.2 41 22.2 41 22.2 42 22.2 43 62.2 44 82 82.2 44 82 82.2 44 82 82.2 44 82 82.2 44 82 82.2 44 82 82.2 44 82 82.2 44 82 82.2 44 82 82.2 44 82 82.2 44 82 82.2 44 82 82.2 44 82 82.2 44 82 82.2 44 82 82.2 44 82 82 82 82 82 82 82 82 82 82 82 82 82	SULT 1 108-545-528D Sequence 1, Patent No. 6 Sequence 1, Patent No. 6 TITLE OF IN PRICH APPLI TYPE: DNA ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: ORGANISM: PRICH CATH SECTION OF IN FILLE REFFERE CURRENT FILL EARLIER APPLE EARLIER APPL

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R APPLICATION NUMBER: 60/048,884
R FILING DATE: 1997-06-06
R FILING DATE: 1997-06-06
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,971
R FILING DATE: 1997-06-06
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PLICATION NUMBER: 60/048,970
LING DATE: 1997-06-06
LICATION NUMBER: 60/048,972
LING DATE: 1997-06-06
FILING DATE: 1997-06-06
APPLICATION WUMBER: 60/048,880
ELING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,896
                                                                                                                      FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/049,020
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,876
FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/048,882
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,899
FILING DATE: 1997-06-06
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LING DATE: 1997-06-06
PPLICATION NUMBER: 60/048,900
LING DATE: 1997-06-06
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LLING DATE: 1997-06-06
PPLICATION NUMBER: 60/048,892
LLING DATE: 1997-06-06
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PPLICATION NUMBER: 60/049,019
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LING DATE: 1997-06-06
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LING DATE: 1997-06-06
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,917
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APPLICATION NUMBER: 60/048,949
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APPLICATION NUMBER: 60/048,974
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,883
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FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,963
FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,878
TLING DATE: 1997-06-06
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APPLICATION NUMBER: 60/092,921
                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/048,895
FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/048,964
FILING DATE: 1997-06-06
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LLING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,897
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APPLICANT: Ronald, Pamela C.
APPLICANT: Wondl, Pamela C.
APPLICANT: Wang, Guo-Liang
APPLICANT: Scabo, Veronique
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: California
COUNTRY: USA
ZIP: 94111-3834
ZIP: 94111-3834
ZIP: 94111-3834
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER: IBM 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Indels
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APPLICATION NUMBER: US/08/567,375 FILING DATE: 29-SEP-1995 FILING DATE: 29-SEP-1995 FILING DATE: US/08/475,891 FILING DATE: US/UN-1995 ATTORNEY/AGRAY INFORMATION: NAME: Bastian, Kevin L. NAME: Bastian, Kevin L. NAME: Bastian, Kevin L. NAME: Bastian, Kevin L. REFERENCE/DOCKET NUMBER: 34,774 REFERENCE/DOCKET NUMBER: US/US/UN-U
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48.2%; Score 24.6; D
Best Local Similarity 70.2%; Pred. No. 15;
Matches 33; Conservative 0; Mismatches
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NAME: CDS
LOCATION: join(1..2676, 3520..3918)
OTHER INFORMATION: /product= "Xa-21"
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3221 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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NUMBER OF SEQ ID NOS: 1227
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 1018
                                                                                                                                                                                                                                            TYPE: DNA; ORGANISM: Homo sapiens
US-09-205-258-15
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US-08-567-375-3

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GENERAL INFORMATION:
APPLICANT: Ronald, Pamela C.
APPLICANT: Wang, Guo-Liang
APPLICANT: Wang, Guo-Liang
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                        3456 ATAAAAAGAACTIGGAIGIATAATIAIGIAAATITACGIGTIAAATAICA 3407
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CTHER INFORMATION: /product= "RRK-B"
CTHER INFORMATION: /product= "RAZ1 Kanthomonas spp. disease
OTHER INFORMATION: resistance gene RRK-B from rice (Oryza
US-08-475-891A-3
                 1 ACAAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCA
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,891A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02370-058910US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                          US-08-475-891A-3/c
; Sequence 3, Application US/08475891A
; Patent No. 5859339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: BARTIAN, KEVIN L.
REGISTRATION NUMBER: 34,774
RELECOMMUNICATION NUMBER: 0237
TELEPONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 68.09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-205-258-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
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                                                                           Gaps
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| Sequence 3, Application US/08587680A
| Sequence 3, Application US/08587680A
| Patent No. 5977434
| GENERAL INFORMATION:
| APPLICANT: Ronald, Pamela C. APPLICANT: Sang, Wen-Yuang
| Procedures and Materials for Conferring
| TITLE OF INVENTION: Disease Resistance in Plants
| NUMBER OF SEQUENCES: 27
| CORRESPONDENCE ADDRESS: 77
| CORRESPONDENCE ADDRESS: 77
| STREES: Two Embarcadero Center, Bighth Floor 77
| CONTRACT OF SEQUENCES: 77
| CONTRACT OF SEQUENCES: 77
| San Francisco Center, Bighth Floor 77
| CONTRACT OF SEQUENCES: 77
| C
                                                                                                                                                                                                       3456 ATAAAAAGAACTTGGATGTATAATTATGTAAATTTACGTGTTAAATATCA 3407
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          Length 3921;
                                                                                                                                         1 ACAAAAAGAAATTGGACTTAAAGTTAAAATACTTTTGTGCTTCAAACATCA
                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/587,680A
Query Match 47.8%; Score 24.4; DB 2; Best Local Similarity 68.0%; Pred. No. 19; Matches 34; Conservative 0; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 24.4; DB 2;
Pred. No. 19;
0; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/587,680A
FILING DATE: 17-JAN-1996
CLASSIFICATION DATA:
CLASSIFICATION BATA:
APPLICATION NUMBER: US/08/373,375
FILING DATE: 17-JAN-1995
FILING DATE: 17-JAN-1995
FILING DATE: 07-JAN-1995
FILING APPLICATION DATA:
APPLICATION NUMBER: US/08/475,891
FILING DATE: 07-JAN-1995
FILING DATE: 29-SEP-1995
FILING DATE: 04-DEC-1995
FILING DATE: 04-DEC-1995
ATTORNEY/AGBNT INFORMATION:
NAME: Bastian, Kevin L,
REGISTATION NUMBER: 34,774
REGISTATION NUMBER: 34,774
RELEEPAR: (415) 576-0300
IELEPHANE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
FURDRANTION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: join(1..2676, 3520..3918)
OTHER INFORMATION: /product= "Xa-21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 68.0%;
Matches 34; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 3921 base pairs
TYPE: nucleic acid
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Gaps

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APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
                                                                                                                                                    EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,881
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
                                                                      CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-19-04
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/048,880
FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/048,899
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,893
FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLING DATE: 1997-06-06
PPLICATION NUMBER: 60/048,892
LLING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60/048,970
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FILING DATE: 1997-06-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/048,962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/048,896
FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/049,020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/048,876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LICATION NUMBER: 60/048,895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/048,894
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FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLICATION NUMBER: 60/048,882
LING DATE: 1997-06-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ILING DATE: 1997-06-06
PPLICATION NUMBER: 60/048,901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/048,915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LICATION NUMBER: 60/049,019
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EARLIER F
EARLIER P
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Pacience 1669, Application US/09976594

Pacent No. 6673549

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS TILLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS CURRENT APPLICATION NUMBER: US/09/976,594

CURRENT FILING DATE: 2001-10-12

NUMBER OF SEC ID NOS: 1143

SOFTWARE: PERL PROGRAM

SEQ ID NO 1069

LENGTH: 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 886, Application US/09976594

Patent No. 6673549
GENERAL INFORMATION:
SPPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: 433-436, 445, 447, 454, 456, 463-465, 472, 495, 498, 662, 939; OTHER INFORMATION: a, t, c, g, or other US-09-976-594-1069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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0
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47.1%; Score 24; DB 4; Length 1856; 68.8%; Pred. No. 24; cive 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 AAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205 AAAAGTAAATGTCCATAAAGCGTTTCACTTATATTCTTCAAACATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 CAAAAAGAAATIGGACTIAAAGTIAAAIACTITIGIGCTICAA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6673549 107309.1
NAME/KEY: unsure
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 23.8; DB Pred. No. 27; 0; Mismatches
                 EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-12-18
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER PRING DATE: 1998-07-15
EARLIER PRING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SEQ ID NO 52
LENGTH: 1856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.7%;
NUMBER:
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Best Local Similarity 72.1
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33; Conservative
                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-205-258-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity
Matches 33; Conserv
  APPLICATION
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US-09-976-594-886/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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OTHER INFORMATION: n equals a, t, c, or NAME/KEY: misc_feature
LOCATION: (713652)...(713652)
OTHER INFORMATION: n equals a, t, c, or
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                            LOCATION: (98343)..(98343)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (103998)...(103998)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
                                                                                                                                                                                                                   NAME/KEY: misor feature
LOCATION: (163385). (163385)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misor feature
LOCATION: (191389). (191389)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misor feature
LOCATION: (191395). (191995)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misor feature
LOCATION: (231380). (231980)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misor feature
LOCATION: (231980). (231980)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misor feature
LOCATION: (234187). (234187)
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LOCATION: (234220)
CUCATION: (234220)
CUTER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (234514). (234814)
CUTER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (305398). (305398)
CUTER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (305418). (305418)
CUTER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (312837). (312837)
CUTER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (312937). (312938)
LOCATION: (312937). (312938)
LOCATION: (312937). (312926)
LOCATION: (31526). (319226)
LOCATION: (559167). (559167)
NAME/KEY: misc feature
LOCATION: (559167). (559167)
CUTER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (559241). (559241)
NAME/KEY: misc feature
LOCATION: (569221). (500992)
CUTER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (569221). (500992)
CUTER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (500992). (00092)
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LOCATION: (622708)..(622708)
OTHER INFORMATION: n equals a, t
NAME/KEY: misc feature
LOCATION: (657081)..(657081)
OTHER INFORMATION: n equals a, t
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,
                                                                                                                                                                          LOCATION: (148948)..(148948)
OTHER INFORMATION: n equals a,
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Patent No. 6503729
GRNERAL INFORMATION:
APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanocod Patent No. 6503729
TITLE OF INVENTION: jannaschii
FILE REFERENCE: PB275
CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
RRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
RNUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1664976
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                                                                                                                                                                                                                                                                                               ) NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6673549 981037.1
US-09-976-594-886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 AAAAAGAAATTGGACTTAAAGTTAAATACTTTTGT 37
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL PROGram
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NAME/KEY:
NAME/KEY:
NAME/KEY:
NOCATION: (28222)
OTHER INPORMATION: n equals a, t, c, or
NAME/KEY: misc feature
LOCATION: (28257)..(28258)
OTHER INPORMATION: n equals a, t, c, or
NAME/KEY: misc feature
LOCATION: (84773)..(84773)
OTHER INFORMATION: n equals a, t, c, or
NAME/KEY: misc feature
LOCATION: (84808)..(84808)
OTHER INFORMATION: n equals a, t, c, or
OTHER INFORMATION: n equals a, t, c, or
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LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals a, t,
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OTHER INFORMATION: n equals a, t,
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LOCATION: (98159)..(98159)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (98239)..(98239)
OTHER INFORMATION: n equals a, t,
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OTHER INFORMATION: n equals a,
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LOCATION: (98266)..(987
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LOCATION: (98120). (981
                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Homo sapiens
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US-08-916-421B-1
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APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOUTWARE: PERL PROGram
SEQ ID NO 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: GUEGLER, Karl et al

ITILE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

FILE REPERENCE: CLOOLOF7

CURRENT APPLICATION NUMBER: US/09/751,389

CURRENT APPLICATION NUMBER: 201-01-02

NUMBER OF SEQ ID NOS: 8

SEQ ID NOS: 8

SEQ ID NO NOS: 8

LENGTH: 786431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             16; Indels
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                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6673549 175918.15
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                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4;
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Pred. No. 43;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 TTAAAGTTAAATACTTTTGTGCTTCAAACATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 23.4;
Pred. No. 65;
                                                                                                                                                                                                                                                                                                                                       LOCATION: 825
COTHER INFORMATION: a, t, c, g, or other US-09-976-594-690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (1)....(786431); OTHER INFORMATION: n = A,T,C or G US-09-751-389-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09751389
Patent No. 6630334
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81.8%;
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Best Local Similarity 67.3%;
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 81.8
Matches 27; Conservative
                                                                                                                                                                                               LENGTH: 6609
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                       NAME/KEY: unsure
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ORGANISM: Human
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US-09-751-389-3/c
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0; Mismatches
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LOCATION: (1664854)..(1664855)
OTHER INFORMATION: n equals a, t, c,
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                                                                                                                                                                                                                                                                                LOCATION: (1084830). (1084830) OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature (1096846). (1096846) OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (1569020)..(1569020)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (1602912)..(1602912)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (1603734)..(1603734)
OTHER INFORMATION: n equals a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: miss feature
LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a, t
NAME/KEY: misc feature
LOCATION: (1313224)..(1313224)
OTHER INFORMATION: n equals a, t
NAME/KEY: misc feature
LOCATION: (1349473)..(1349473)
OTHER INFORMATION: n equals a, t
NAME/KEY: misc feature
                                                                                                                                                                                                                      LOCATION: (871619)..(871619)
OTHER INFORMATION: n equals a,
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LOCATION: (1119881)..(1119881)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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LOCATION: (1470091)..(1470091)
OTHER INFORMATION: n equals a,
                                                                                                                                                      NAME/KEY: misc feature
LOCATION: (855539). (855539)
OTHER INFORMATION: n equals a,
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    LOCATION: (741684)..(741684)
OTHER INFORMATION: n equals a,
                                                       LOCATION: (779455)...(779455)
OTHER INFORMATION: n equals a,
NAME/KEY: misc feature
LOCATION: (779676)...(779676)
OTHER INFORMATION: n equals a,
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                                           NAME/KEY: misc feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

Sequence 1552, Application US/09328352 Patent No. 6562958

US-09-328-352-1552

555193 AAAAGAAAATTAATCATGCAAATATATATTTAATGCATCAAACATTAT 555243

Sequence 690, Application US/09976594 Patent No. 6673549 PARRAL INFORMATION: APPLICANT: Furness, Michael

RESULT 10 US-09-976-594-690/c

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FILE REFERENCE: GTC99-03PA CURRENT APPLICATION NUMBER: US/09/328,352

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APPLICANT: Lagace, Robert, E.
APPLICANT: Patterson, Chandra
APPLICANT: Patterson, L.
TITLE OF INVENTION: NUCLECTION SEQUENCES OF MORAXELLA CATARRHALIS GENOME
FILE REFERENCE: PM-0008-4 US
CURRENT APPLICATION NUMBER: US/09/596,002
CURRENT FILING DATE: 2000-06-16
PRIOR PAPLICATION NUMBER: 60/140,121
PRIOR PLING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PERL Program
SEQ ID NO 10
LENGTH: 19988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1287 AATCCAAAAAGGCTTTAATTTTAATTTCTTTGTTGCATAAAATATCA 1241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Length 19988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 AAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature

; OTHER INFORMATION: Incyte template ID No., 6632636 10

; PUBLICATION INFORMATION:

US-09-596-002-10
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Pred. No. 65;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7, 2004, 15:44:33
                                                                                         Sequence 10, Application US/09596002; Patent No. 6632636
GENERAL INFORMATION: APPLICANT: Lagace, Robert, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45.1%;
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Best Local Similarity 68.1
Matches 32, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: M. catarrhalis
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: May 7 Job time: 34.6094 secs
                                               RESULT 15
US-09-596-002-10/c
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Batent No. 6673910
Batent No. 6673910
Batent No. 673910
Batent No. 673910

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR

TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: 2709. 2005-001

CURRENT APPLICATION NUMBER: US/09/540,236

CURRENT PILING DATE: 2000-04-04

NUMBER OF SEQ ID NOS: 3840

SEQ ID NO 1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: LYAIN DOUGETTE-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: BYDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674
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                                                                                                                                                                                                                                                                                                                                   263 ATATTAATGAAGTGGACTTAAATGTACGTCCTTTTGTTCTTAAA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 AAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCA
                                                                                                                                                                                                                                       13; Indels
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                                                                                                                                                                                        Query Match
45.5%; Score 23.2; Di
Best Local Similarity 70.5%; Pred. No. 42;
Matches 31; Conservative 0; Mismatches
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45.5%; Score 23.2;
Best Local Similarity 77.8%; Pred. No. 43
Matches 28; Conservative 0; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1278, Application US/09134001C Patent No. 6380370 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA; CRGANISM: Staphylococcus epidermidis
US-09-134-001C-1278
                                                                                         TYPE: DNA; CRGANISM: Acinetobacter baumannii
US-09-328-352-1552
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 1552
LENGTH: 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 68.1'
Matches 32; Conservative
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US-09-540-236-1082
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US-09-540-236-1082/c
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Gaps

0

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                  Copyright
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- nucleic search, using sw model OM nucleic

May Run on:

7, 2004, 11:56:28 ; Search time 104.189 Seconds (without alignments) 2079.475 Million cell updates/sec

US-10-071-411A-1_COPY_450_500 Title:

1 acaaaaagaaattggactta.....ttttgtgcttcaaacatcat Perfect score: Sequence:

51

IDENTITY NUC Scoring table:

Gapop 10.0 , Gapext 1.0

3373863 seqs, 2124099041 residues

Searched:

6747720 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 99% Listing first 45 summaries

geneseqn2001bs:* geneseqn2002s:* geneseqn2003as:* N_Geneseq_29Jan04:* geneseqn2001as:* geneseqn2003bs:* geneseqn2003cs:* geneseqn1980s:* geneseqn1990s:* geneseqn2000s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004s:*

CTIMMADITE

	Description	Abt11173 Human 5-1		Abl32116 Human imm	7				Abl70131 Chemicall	Aca39547 Prokaryot	Acc69139 M. genita	Continuation (6 of	Continuation (5 of	Aai83146 Human pol	Abl33441 Human imm	Abl54362 Chemicall	Adc87621 Human GPC	Abv58521 Human pro	Aak81112 Human imm	Aaz93368 Seguence	Aal41059 cDNA of H	Abk41870 cDNA enco	Adb59537 Connectiv	Aac80574 Human sec
SUMMARIES	ID	ABT11173	ABT11114	ABL32116	ABL32117	ABK31177	ABK31176	ABL70132	ABL70131	ACA39547	ACC69139	AAT58840 5	AAT58840_4	AA183146	ABL33441	ABL54362	ADC87621	ABV58521	AAK81112	AAZ93368	AAL41059	ABK41870	ADB59537	AAC80574
	DB	9	9	9	v	ø	9	9	9	7	7	~	7	4	9	9	6	S	4	ო	9	4	æ	М
	Length DB	168174	168273	13249	13249	13249	13249	13249	13249	879	10809	80073	110000	355	5864	5864	349938	607	206	1214	1214	1285	1285	1779
•	* Query Match	94.1	94.1	75.3	75.3	75.3	75.3	75.3	75.3	56.1	56.1	56.1	56.1	51.8	50.2	50.2	50.2	49.B	49.4	49.4	49.4	49.4	49.4	49.4
	Score	4.8	48	38.4	38.4	38.4	38.4	38.4	38.4	28.6	28.6	28.6	28.6	26.4	25.6	25.6	25.6	25.4	25.2	25.2	25.2	25.2	25.2	25.2
	Result No.		2	ო	ი 4	G 5	9	0 7	80	თ	c 10	11	12	c 13	c 14	c 15	c 16	17	18	c 19	c 20	~	c 25	23

Aak81109 Human imm	Aak81111 Human imm	Aak81110 Human imm	Abl34006 Human imm	Abl17308 Drosophil	Abl33240 Human imm	Continuation (2 of	Acd13446 Human DNA	Aai81019 Human pol	Abk72766 Bacillus	Aav84415 Human sec	Aba83198 Human sec	Ach04699 Novel hum	Acd44509 Human cDN	Abk73006 Bacillus	Aak78949 Human imm	Aad48267 Ehrlichia	Abl33138 Human imm	Aal04782 Human rep	Abl97677 Human tes	Ada02576 Human FKB	Adb72314 Human FKB
AAK81109	AAK81111	AAK81110	ABL34006	ABL17308	ABL33240	AAL52246 1	ACD13446	AA181019	ABK72766	AAV84415	ABA83198	ACH04699	ACD44509	ABK73006	AAK78949	AAD48267	ABL33138	AAL04782	ABL97677	ADA02576	ADB72314
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5728	5733	5733	18434	4129	9888	110000	240000	446	948	1018	1018	1018	1018	1218	3982	4460	5678	22927	22927	87878	87878
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49	49	49	49	49	49	49	49	48	48	48	48	48	48	48	48	48	48	48	48	48	48
25.2	25.2	25.2	25.2	25	25	25	25	24.6	24.6	24.6	24.6	24.6	24.6	24.6	24.6		24.6		24.6	24.6	24.6
24	22	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

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Human, polymorphic region, 5-lipoxygenase, 5-LO gene; asthma, bronchitis, sinusitis; ulcerative colitis; nephritis; amyloidosis; sarcoidosis; rheumatoid arthritis; scleroderma; lupus, non-allergic rhinitis; polymyositis; Reiter's syndrome; pocifisis; pelvic inflammatory disease; atopic; contact dermatitis; forensic medicine; paternity testing; enzyme;
                                                                    Human 5-lipoxygenase gene related DNA sequence SEQ ID No 63.
                BP.
                ABT11173 standard; DNA; 168174
                                                  (first entry)
                                                  05-DEC-2002
                                  ABT11173;
RESULT 1
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Homo sapiens.

WO200262825-A2.

15-AUG-2002.

07-FEB-2002; 2002WO-US003546.

08-FEB-2001; 2001US-0267515P. 21-AUG-2001; 2001US-0314248P.

(MILL-) MILLENNIUM PHARM INC.

Meyer J; Barnes G,

WPI; 2002-627522/67.

New isolated nucleic acid molecule with an allelic variant of a polymorphic region of an 5-LO gene, useful for diagnosing and/or prognosticating disorders associated with an aberrant inflammatory response such as asthma.

Disclosure; Fig 4; 290pp; English.

The invention relates to an isolated human nucleic acid molecule comprising an allelic variant of a polymorphic region of a 5-lipoxygenase (5-LO) gent, where the allelic variant comprises one or more nuclectide selected from any of 3, 20 or 20 parts sequences, given in the specification, or their complement. The compositions and methods of the

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associated with an aberrant inflammatory response such as asthma, bronchitis, sinualis, ulcerative colitis, nephritis, amyloidosis, rheumatoid arthritis, aarcoidosis, scleroderma, lupus, non-allergic rhinitis, polymyositis, Reiter's syndrome, psoriasis, pelvic inflammatory disease, atopic and contact dermatitis. The nucleic acid molecules can also be useful for identifying an individual amongst other individuals from the same species for use in forensic medicine and paternity testing. This polymucleotide sequence represents DNA relating to the human 5-lipoxygenase (5-LO) gene of the invention
present invention are useful for diagnosing and/or prognosing disorders
8888888888888
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Sequence 168174 BP; 46808 A; 36442 C; 36942 G; 46474 T; 0 U; 1508 Other;

ö Gaps ö Length 168174; 4 AAAAGAAATIGGACTIAAAGTIAAATACTITITGIGCTICAAACAICAI Indels 94.1%; Score 48; DB 6; Li 100.0%; Pred. No. 8.9e-06; 100.0%; Pred. No. Conservative Local Similarity es 48; Conserv Query Match Best Loc Matches

ABT11114 standard; DNA; 168273 ABT11114; RESULT 2

BP

(first entry) 05-DEC-2002

Human 5-lipoxygenase gene related DNA sequence SEQ ID No 2.

polymorphic region; 5-lipoxygenase; 5-LO gene; asthma; bronchitis; sinusitis; ulcerative colitis; nephritis; amyloidosis; sarcoidosis; hemmatoid arthritis; scleroderma; lupus; non-allergic rhinitis; polymyositis; Reiter's syndrome; psociasis; pelvic inflammatory disease; atopic; contact dermatitis; forensic medicine; paternity testing; enzyme; Human:

Homo sapiens.

WO200262825-A2

15-AUG-2002.

07-FEB-2002; 2002WO-US003546

08-FEB-2001; 2001US-0267515P. 21-AUG-2001; 2001US-0314248P.

(MILL-) MILLENNIUM PHARM INC.

Meyer J; Barnes G, WPI; 2002-627522/67.

New isolated nucleic acid molecule with an allelic variant of a polymorphic region of an 5-LO gene, useful for diagnosing and/or prognosticating disorders associated with an aberrant inflammatory response such as asthma

Disclosure, Fig 2; 290pp; English.

comparising an allelic variant of a polymorphic region of a 5-lipoxygenase (5-LO) gene, where the allelic variant comprises one or more nucleotide selected from any of 3, 20 or 21 base pair sequences, given in the specification, or their complement. The compositions and methods of the present invention are useful for diagnosing and/or prognosing disorders associated with an aberrant inflammatory response such as asthma, bronchitis, sinusitis, ulcerative colitis, nephritis, amyloidosis, rheumatoid arthritis, sarcoidosis, scleroderma, lupus, non-allergic rhinitis, polymyositis, Reiter's syndrome, psoriasis, pelvic inflammatory The invention relates to an isolated human nucleic acid molecule

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders,
                 also be useful for identifying an individual amongst other individuals from the same species for use in forensic medicine and paternity testing. This polynuclectide sequence represents DNA relating to the human 5-lipoxygenase (5-LO) gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiarteriosclerotic; antianaemic; cytostatic; noctropic; neuroprotective; anti-HIV; anticonvuleant; ophthalmological; antirheumatic; antiartic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                         Sequence 168273 BP; 46834 A; 36467 C; 36966 G; 46498 T; 0 U; 1508 Other;
disease, atopic and contact dermatitis. The nucleic acid molecules can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acute myeloid
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloi leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                            166921 AAAAGAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT 166968
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                                                                                                                                                  Length 168273;
                                                                                                                                                                                                                           4 AAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT
                                                                                                                                                                                      Indels
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                                                                                                                                                DB 6; Le:
8.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immune system associated gene SEQ ID NO:
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100.0%; Pred. No. c...
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01-SEP-2000; 2000DE-01043826.
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                                                                                                                                                                                      48; Conservative
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Best Local Similarity
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Matches
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                                                                                                                                                                                                                                                                                                                   RESULT 3
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Human;

RESULT 4

à d

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signal transduction associated genes. The DNA sequences are chemically modified using a solution of bisulphite, hydrogen sulphite or disulphite. Also disclosed are oligonucleotides and/or PNA oligomers for detecting the cytosine methylation state (pgd islands) of these genes, and a method of or the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with signal transduction. The genomic DNA can be obtained from cells or cellular components which contain DNA, e.g. cell innes, bloopises, blood, sputum, stool, urine, cerebral-spinal fluid, tissue embedded in paraffin such as tissue from eyes, intestine, kidney, brain, heart, prostate, lung, breast or liver, histologic object slides, and all their possible combinations. The sequences of the invention are useful for the diagnosis and therapy of diseases associated with signal transduction, or their complementary sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                     Human, signal transduction associated gene, cytosine methylation state;
CpG island, signal transduction associated disease; solid tumour; cancer;
antitumour; cytostatic; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic sequences of genes associated with signal transduction.
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                                                                 Signal transduction associated gene modified complementary DNA #10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75.3%; Score 38.4; DB 6; ilarity 87.5%; Pred. No. 0.0082; Conservative 0; Mismatches 6
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01-SEP-2000; 2000DE-01043826.
                     (first entry)
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es 42; Conserv
                                                                                                                                                                                                                                                                         WO200200926-A2
                                                                                                                                                                                                        Homo sapiens
                     23-APR-2002
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                                                                                                                                                                                                                                Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, Albo, epilepsy, neurofibromatosis, rheumacoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid comprising fragment of chemically modified gene, useful diagnosis and treatment of diseases associated with abnormal cytosine
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                                                                                                                                                                                                                                                                                                                                                                                        antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease, arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                     system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13249 BP; 3128 A; 273 C; 3397 G; 6451 T; 0 U; 0 Other;
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                     4 AAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 AAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 90; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                     Human immune system associated gene SEQ ID NO: 90.
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Pred. No. 0.0082;
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01-SEP-2000; 2000DE-01043826.
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87.5%;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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0,

Gaps

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Indels

6; Length 13249;

9541

Signal transduction associated gene modified DNA #10.

(first entry)

23-APR-2002

ABK31177 standard; DNA; 13249 BP.

ABK31177;

ABK31177/c ID ABK311 XX AC ABK311

RESULT 5

g ⋧

Matches

51

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Cell signalling; cytosine methylation; cell signalling disease; cancer; tumour; cytostatic; ds.
                                                                                                                                                                                                                Chemically treated cell signalling DNA sequence complementary to#11.
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Library in transduction related genes. The DNA sequences are chemically modified using a solution of bigulphite, hydrogen sulphite or disulphite. Also disclosed are oligonucletides and/or PNA oligoners for detecting the cytosine methylation state (CPG islands) of these genes, and a method for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with signal transduction. The genomic DNA, e.g. cell ines, biopsies, blood, sputum, stool, urine, cerebral-spinal fluid, lines, biopsies, blood, sputum, stool, urine, cerebral-spinal fluid, brain, heart, prostate, lung, breast or liver, histologic object slides, and all their possible combinations. The sequences of the invention are useful for the diagnosis and cherapy of diseases associated with signal transduction e.g. solid tunours and cancer. ABK31158-ABK31545 represent chemically pretreated genomic DNA sequences of different genes associated with signal transduction, or their complementary sequences. Note: The sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequences. Note: The sequence data for this patent did not form part of the printed sequence.
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                     Human, signal transduction associated gene; cytosine methylation state; CpG island; signal transduction associated disease; solid tumour; cancer; antitumour; cytostatic; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonuclectide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic sequences of genes associated with signal transduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to chemically modified DNA sequences of
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Pred. No. 0.0082;
0; Mismatches 6
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87.5%;
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01-SEP-2000; 2000DE-01043826.
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Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                           WO200200926-A2.
                                                                                                                          sapiens
                                                                                                                                                                                                                                      03-JAN-2002
                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                             olek A,
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The invention relates to a nucleic acid comprising a sequence of at least the bases of a segment of chemically pretreated DNA of genes associated with cell signalling. The activity of the modified sequences of the invention may be described as cytostatic. The object of the invention is to provide the chemically modified DNA of genes associated with cell signalling, as well as to oligonucleotides and/or bNA-oligoners for detecting cytosine methylations, as well as a method which is particularly suitable for the diagnosis and/or therapy of genetic and parameters of genes associated with cell signalling. The chemically modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as solid tumours and cancer. The sequences given in records ABL70111-AB170626 represent chemically pre-treated genomic DNA's of genes associated with cell signalling. Note: The sequence data for this patent is not represented in the printed sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the

European Patent Office

Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signaling e.g. cancer, comprises chemically modified genomic sequences of genes associated with cell signaling.

Berlin K;

Olek A, Piepenbrock C,

WPI; 2002-154758/20.

(EPIG-) EPIGENOMICS AG

29-JUN-2001; 2001WO-EP007471.

WO200202807-A2

10-JAN-2002.

Unidentified.

30-JUN-2000; 2000DE-01032529. 01-SEP-2000; 2000DE-01043826.

Claim 1; SEQ ID NO 22; 24pp + Sequence Listing; English

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ó,
                                                                                                                                                                                                                                                            Cell signalling, cytosine methylation, cell signalling disease; cancer; tumour; cytostatic; ds.
                                                 Gaps
Sequence 13249 BP; 3128 A; 273 C; 3397 G; 6451 T; 0 U; 0 Other;
                       Score 38.4; DB 6; Length 13249;
Pred. No. 0.0082;
0; Mismatches 6; Indels 0;
                                                                                                21
                                                                        4 AAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT
                                                                                                                                                                                                                                       Chemically treated cell signalling DNA sequence#11.
                                                 0; Mismatches
                                                                                                                                                               ABL70131 standard; DNA; 13249 BP
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                        Query Match
Best Local Similarity 87.5%;
Matches 42; Conservative
                                                                                                                                                                                                               01-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                             WO200202807-A2
                                                                                                                                                                                                                                                                                                    Unidentified
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                                                                                                                                         RESULT 8
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(first entry)

WPI; 2003-029926/02.

comprises chemically modified genomic

Berlin K;

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The invention relates to a nucleic acid comprising a sequence of at least 18 bases of a segment of chemically pretreated DNA of genes associated with cell signalling. The activity of the modified sequences of the invention may be described as cytostatic. The object of the invention is to provide the chemically modified DNA of genes associated with cell signalling, as well as oligonucleotides and/or PNA-oligoners for detecting cytosine methylations, as well as a method which is particularly suitable for the diagnosis and/or therapy of genetic and parameters of genes associated with cell signalling. The chemically modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as solid tumours and cancer. The sequences given in records ABL70111-ABL70626 represent chemically pre-treated genomic DNA's of genes associated with cell signalling. Note: The sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the
                                                                                                                                                                                                                                                                                      Nucleic acid, useful for diagnosis and therapy of diseases associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13249 BP; 3594 A; 273 C; 3130 G; 6252 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense; ds; prokaryotic essential gene; cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 AAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 21; 24pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                           with cell signaling e.g. cancer, comprises chemica
sequences of genes associated with cell signaling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prokaryotic essential gene #21204.
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06-SEP-2001; 2001US-00948993.
25-0CT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
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1 Similarity 87.5%;
42; Conservative (
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01-SEP-2000; 2000DE-01043826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JUN-2003 (first entry)
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                                                                                                                                             Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   European Patent Office
                                                                      (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycoplasma genitalium.
                                                                                                                                                                                                                   WPI; 2002-154758/20
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200277183-A2.
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                                                                                                                                                olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACA39547/c
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Gaps

0;

6; Indels

Score 38.4; DB 6; Pred. No. 0.0082; 0; Mismatches 6;

ВР

Length 13249;

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the inventor relates by the control of a cell. Also included are:

(1) a vector comprising a prodiferation of a cell. Also included are:

(1) a vector comprising a prodiferation of a cell. Also included are:

(2) a vector comprising a promoter operably linked to the mucleic acid

(3) an isolated control of a cell ontaining the vector; (3) an isolated are:

(4) a vector comprising a promoter operably linked by the antisense mucleic acid; (4) an antibody capable of specifically binding antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the cartistic or the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operan required for proliferation, (7) identifying a compound that influences the activity of required for proliferation, or that has an activity against a biological pathway in which a proliferation required gene or the biological pathway in which a proliferation required gene or the biological pathway in which a proliferation required gene or the biological pathway in which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) prolifing a compound's activity; (11) a culture comprising strains in which the extent compound's activity; (11) a culture comprising strains in which the extent compound's activity; (12) determining the extent convolute acids required convoluted are useful for proliferation of an organism. The antisense nucleic acids are useful for for a dentifying proteins or screening for homologous nucleic acids required for containing and actional actional acids are useful for formal and acids are useful for formal and account and actional accidence of a compound accidence of a contain and 
                                                                                                                   New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycoplasma genitalium; gene cassette; replication; transcription; translation; metabolism; basic genetic operating system; gene therapy; autonomous prototrophic nanomachine; auxotrophic nanomachine; nanomachine; bioreactor; bioremediation; therapputic, delivery system; artificial tissue; artificial organ system; energy conversion system; processing system; anabolic system; catabolic system; biological coating; cosmetic; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           537 acraaaaggarriggaargaaagragaaracrirrirccriraacagraar 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ACAAAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M. genitalium aerobic metabolism gene cassette DNA SEQ ID NO:7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
56.1%; Score 28.6; DB 7; Length 879;
Best Local Similarity 72.5%; Pred. No. 8.8;
Matches 37; Conservative 0; Mismatches 14; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 879 BP; 269 A; 120 C; 143 G; 347 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                Claim 14; SEQ ID NO 27417; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                            P-PSDB; ABU35677
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Zyskind JW; Xu HH;

Ohlsen KL, Forsyth RA,

Haselbeck R, Yamamoto R,

Malone C, Carr GJ,

Zamudio C, Trawick JD,

Wang L, Wall D,

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Gaps

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14; Indels

DB 2; Length 110000;

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AAT58840 from base 400001 (Mycoplasma genitalium genome. ) fragments LOCUS AAT58840 Accession Aat58840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to human polynucleotides (AA179941-AA193841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoissis regulating activity and may be useful in the diagnosts and/or activity and may be useful in the diagnosts and/or activity and may be useful in the diagnosts and/or activity and activity and activity and activity and activity and may be useful in the diagnosts and/or activity and activity and may be useful in the diagnosts and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                     108476 ACTAAAAGGATTTGGAATGAAACTAGAATACTTTTTTCCTTTAACAGTAAT 108526
                                              LOCUS AAT58840 Accession Aat58840
End
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 3206; 1399pp + Sequence Listing; English
                                                                                                                                                                                                                                     Score 28.6; DB Pred. No. 12; 0; Mismatches
                                                                                                                      210000
310000
410000
510000
                                                                                                     110000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human polynucleotide SEQ ID NO 3206.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAI83146 standard; cDNA; 355 BP
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                                                                                                                                                                                                                                          56.1%;
72.5%;
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400001
500001
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                                              o of
                                                                                                                                                                                                                                                              Similarity 37; Conserv
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                            AAT58840 4
Continuation (5 of 6) o
WP Sequence split into
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                                                                                     Fragment Name
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                                                                                                                   AAT58840_1
AAT58840_2
AAT58840_3
AAT58840_4
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
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AAT58840 5

AAT58840 6 of 6) of AAT58840 from base 500001 (Mycoplasma genitalium genome. Continuation (6 of 6) of AAT58840 from AAT58840 Accession Aat58840 WP AAT58840 1 100000 WP AAT58840 1 100001 210000 WP AAT58840 2 200001 310000 WP AAT58840 3 300001 410000 WP AAT58840 4 400001 510000 WP AAT58840 5 50001 50000
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                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a basic genetic operating system for an autonomous prototrophic or auxotrophic nanomachine comprising a minimal gene set sufficient for viability or replication, optionally in the presence of an auxotrophic molecule. Also described is an autonomous prototrophic or auxotrophic molecule. Or auxotrophic molecule comprising a basic genetic operating system for autonomous prototrophic or auxotrophic molecule, and a particle envelope. The nanomachines used in gene therapy. The basic genetic operating system or nanomachine is useful in therapeutic, diagnostic and industrial applications, e.g. as bloreactor, for biopremediation, for the production of a therapeutic biomolecule or as a therapeutic reagent, for the production of a diagnostic indicator or reagent, as a delivery system, as an artificial diagnostic indicator or reagent, as a delivery system, as an artificial
                                                                                                                                                                                                                                                                New basic genetic operating system for autonomous prototrophic or auxotrophic nanomachine, useful for therapeutic, diagnostic or industrial purposes, comprises a nanomachine genome encoding a gene set for viability or replication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue or organ system, as an energy conversion system, as a processing system, as an anabolic or catabolic system, for the production of biological films or coatings, and for cosmetic applications. The present sequence represents a Mycoplasma genitalium gene cassette nucleotide sequence, which is used in an example from the present invention for the design and synthesis of a basic genetic operation system for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 28.6; DB Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 210-213; 250pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              replication competent nanomachine
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Best Local Similarity 72.5%;
Matches 37; Conservative
                                                                           18-SEP-2002; 2002WO-US029811
                                                                                                             20-SEP-2001; 2001US-00960870
                                                                                                                                                      (EGEA-) EGEA BIOSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 72.5
Matches 37; Conservative
                                                                                                                                                                                                                               WPI; 2003-354602/33
WO2003025145-A2
                                      27-MAR-2003
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                                                                                                                                                                                           Evans GA;
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syndrome; cardiopathy; neurodegenerative disorder; renal ischaemia; amyotrophic lateral sclerosis;

06-APR-2001; 2001WO-EP003969

WO200177164-A2 Unidentified

18-OCT-2001

Chemically treated apoptosis gene complementary to gene #31.

Apoptosis; HIV; Bloom Herpes simplex virus;

cancer; ds.

entry)

(first

29-JUL-2002

ABL54362;

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Gaps

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BP.

ABL54362 standard; DNA; 5864

RESULT 15 ABL54362,

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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid reukaemia, Alzhaimer's disease, Alzhailepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                    antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid comprising fragment of chemically modified gene, useful idiagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                      immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5864 BP; 1601 A; 136 C; 1351 G; 2776 T; 0 U; 0 Other;
                                 Length 355;
                                                                                                                                    209 aradarriggacrradaarrcadaacrcrrgcccrrradadagaca 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 1414; 32pp + Sequence Listing; German.
                                                                    Indels
                                                                                                     7 AGAAATIGGACTIAAAGTIAAAIACTITIGIGCTICAAACAICA 50
Sequence 355 BP; 86 A; 65 C; 74 G; 130 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                  Human immune system associated gene SEQ ID NO: 1414.
                                                                  11;
                                   DB 4;
                                                 75.0%; Pred. No. 41; ive 0; Mismatches
                                   Score 26.4;
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                                                                                                                                                                                                                               BP
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01-SEP-2000; 2000DE-01043826.
                                                                                                                                                                                                                               ABL33441 standard; DNA; 5864
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                                   51.8%;
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                                                                    Conservative
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                                                     Local Similarity
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                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chemically modified sequences of genes associated with apoptosis useful to determine methylation patterns of genomic DNA samples fidiagnosis of associated diseases such as cancer.
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70.8%; Pred. No. 89;
tive 0; Mismatches
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time: 111.189 secs
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                                                                                                                                                                                                                                                                                                                                                                                                   Berlin K;
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07-APR-2000; 2000DE-01019173.
30-UUN-2000; 2000DE-01035529.
01-SEP-2000; 2000DE-01043826.
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Matches 34; Conservative
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14; Indels

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34; Conservative

Matches

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Query Match Best Local Similarity

48

DB 6; Length 5864;

ACAAAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACAT

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(without alignments)
4157.648 Million cell updates/sec
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1 acaaaaagaaattggactta......ttttgtgcttcaaacatcat 51
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

RESULT 1

AL731567 LOCUS DEFINITION ACCESSION	AL731567 129266 bp DNA linear PRI 20-JUN-2002 Human DNA sequence from clone RP11-67C2 on chromosome 10, complete sequence. AL731567 AC010865 AL731567 AC GI.2157524
KEYWORDS SOURCE ORGANISM	HTG. HOMO sapiens (human) HOMO sapiens Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE AUTHORS TITLE	1 (bases 1 to 129266) Whitehead, S. Direct Submission

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23771:
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                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                   COMMENT
                                                                                                                                                                      Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequence submission only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw:, SWISSPROT; Tr:, TREMBL; WORMPEP; Information on the WORMPEP database can be found at the subclosure that their source databases:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Diren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Balren, B., Linton, L., Nusbaum, C., Lander, E., Boukhgalter, B., Barowh, A., Castle, A., Cangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RPII-67C2 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (bases I to 160654)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens, clone RP11-16P14
                                                                                                                                         http://www.genomecorp.com
During sequence assembly data is compared from overlapping clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr10
Submitted (31-MAY-2002) Wellcome Trust Sanger Institute, Hinxton,
                   Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jun 21, 2002 this sequence version replaced gi:21213582.
Draft Sequence Produced by Genome Therapeutics Corp, 100 Beaver
Street, Waltham, MA 02453, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 0.00039;
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/clone_lib="RPCI-11.1"
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HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
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Perreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Hadord, A., Horton, L., Howland, J. C., Johnson, R., Grant, G., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Maddonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylon, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Soy, A., Sartos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M., Wheeler, J., Wu, X., Direct Submission
                                                                                                                                                                                                                                                                                                                                Submitted (15-007-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 14, 2000 this sequence version replaced gi:6524208.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 30 conigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Sequencing vector: M13, M77815, 100% of reads
Sequencing vector: M13, M77815, 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 111055 bases at least Q30
Consensus quality: 115066 bases at least Q30
Consensus quality: 147921 bases at least Q20
Insert size: 163000; agarose-fp
Insert size: 157754; sum-of-contigs
Quality coverage: 2.9 in Q20 bases; sum-of-contigs
Quality coverage: 3.0 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------- Project_Information
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gap of 100 bp
contig of 1209 bp in length
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contig of 1551 bp in length
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contig of 2311 bp in length
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Direct Submission
Submitted (25-SEP-1999) Genome Therapeutics Corporation, 100 Beaver
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Homo sapiens chromosome 06 clone RP11-326D18, WORKING DRAFT
SEQUENCE, 25 unordered pieces.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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On Sep 1, 2000 this sequence version replaced gi:8247773
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ACO10862.7 GI:9957987
HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_CANCELLED.
Homo sapiens (human)
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94.1%; Score 48; DB 2; L
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 48; Conservative 0; Mismatches 0;
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Smith, D.R.
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3: contig of 10249 bp in length
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              Consensus quality: 162991 bases at least Q40 Consensus quality: 176452 bases at least Q30 Consensus quality: 179870 bases at least Q30 Insert size: 129533; sum-of-contigs Quality coverage: 4.2x in Q20 bases; sum-of-contigs
                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 25 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
version 990315
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/clone="RP11-326D18"
/clone_lib="RPCI-11"
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Diagnosis of diseases associated with signal transduction
Patent: WO 0200926-A 20 03-JAN-2002;
Epigenomics AG (DE)
Location/Qualifiers
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Diagnosis of diseases associated with signal transduction
Patent: WO 0200926-A 19 03-JAN-2002;
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AX344173
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Sequence 19 from Patent W00200926.
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PAT 06-FEB-2002

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DEFINITION

RESULT 6 AX345018 LOCUS

ACCESSION VERSION KEYWORDS

ORGANISM

SOURCE

REFERENCE AUTHORS

TITLE JOURNAL

FEATURES

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (23-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
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/db xref="taxon:35450"
/noTe="chemically treated genomic DNA (Homo sapiens)"
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1. .13249
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/organism="synthetic DNA"
/mol_type="unassigned DNA"
/db xref="taxon:32630"
/noTe="chemically treated genomic DNA (Homo sapiens)"
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Human DNA sequence from clone RPI1-394I23 on chromosome
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Diagnosis of diseases associated with cell signalling
Patent: WO 02007-A 22 10-JAN-2002;
Epigenomics AG (DE)
Location/Qualifiers
                                                     olek,A., Piepenbrock,C. and Berlin,K. Diagnosis of diseases associated with cell signalling Patent: WO 0202807-A 21 10-JAN-2002; Epigenomics AG (DE)
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.larity 87.5%; Pred. No. 0.33;
Conservative 0; Mismatches
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nes 42; Conserv
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db xref="taxon:32630"
/noTe="chemically treated genomic DNA (Homo sapiens)"
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                                                                                                                                                                                                                             Olek,A., Piepenbrock,C. and Berlin,K. Diagnosis of diseases associated with the immune system Patent: WO 0200928-A 89 03-JAN-2002; Epigenomics AG (DE)
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llarity 87.5%; Pred. No. 0.33;
Conservative 0; Mismatches
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Sequence 21 from Patent W00202807.
                                                         AX345018 13249 bp
Sequence 89 from Patent W00200928.
AX345018
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Sequence 90 from Patent WO0200928.
AX345019
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Matches 42; Conserv
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Best Local Simi
Matches 42;
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RESULT 7 AX345019/c

LOCUS

ACCESSION VERSION

KEYWORDS

SOURCE ORGANISM

REFERENCE AUTHORS

JOURNAL

TITLE

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Gaps

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Indels

source

FEATURES

DEFINITION ACCESSION VERSION KEYWORDS SOURCE

RESULT 8 AX348563 LOCUS

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23-AUG-2001 10,

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Consensus quality: 18669 bases at least Q40
Consensus quality: 12596 bases at least Q30
Guality coverage: 4.18 in Q20 bases; pulse field gel estimation.
Quality coverage: 4.18 in Q20 bases; pulse field gel estimation.
VNDE: This is a working draft's sequence. It currently consists of 16 contids. Gaps between the contigs estimation.
* NOTE: This is a working draft's sequence. It currently consists of 16 contids. Gaps between the contigs estimation.
* In this is a working draft's sequence. It currently consists of 16 contids. Gaps between the contigs estimation.
* This is equence will be preserved.
* This sequence will be preserved.
* This
Submitted (14-MAR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jul 18, 2000 this sequence version replaced gi:7711854.
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/clone_lib="CalTech human BAC library D"
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0; Mismatches
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/organism="Homo sapiens"
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                                                                                                     -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
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chromosome="5"
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                                                                                                                                                                                                                                                                   Project Information
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                                                                          COMMENT
requests: clonerequest@sanger.ac.uk
On Aug 31, 2001 this sequence version replaced gi:14268248.
During sequence assembly data is compared from overlapping clones.
Mhere differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the vortation amnotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em.; EMBL; Sw.; SWISSEROT; Tr.; TREMBL; WORMPEP; Information on the WORMPEP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128529 bp DNA linear HTG 18-JUL-2000 SEQUENCE, 16 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RPDATANT: This sequence is not the entire insert of clone RP11-394I23 It may be shorter because we sequence overlapping sections only once, except for a short overlap.

The true right end of clone RP11-394I23 is at 192044 in this sequence. The true left end of clone RP11-657A9 is at 85254 in this sequence. The true right end of clone RP11-3945 is at 100 in this
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.sanger.ac.uk/HGP/Chr10
RP11-394123 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 128529)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
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Sequencing of Human Chromosome 5
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/db_xref="taxon:9606"
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/clone="RP11-394I23"
/clone_lib="RPCI-11.2"
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HTG; HTGS_PHASE2; HTGS_DRAFT.
Homo sapiens (human)
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Submitted (16-MAY-2003) Shih-Feng Tsai, National Health Research Institutes (NHRI), Division of Molecular and Genomic Medicine; 128, Yen-Chiu-Yuan Road, Sec 2, Taipel 115, Taiwan
Yen-Chiu-Yuan Road, Sec 2, Taipel 115, Taiwan
Tel:886-2-28267319, Fax:886-2-28200552)
The Chimpanzee Chronosome 22 Sequencing Consortium consists of:
*Chimpanzee Chronosome 22 Sequencing Consortium consists of:
*Chimpanzee Chronosome 22 Sequencing Consortium consists of:
*Chimpanzee Chronosome Center at Shanghai, Shanghai, China;
*CBF, Dept. of Genome Analysis, Braunschweig, Germany; *Institute
of Molecular Biotechnology, Jena, Germany; *KRIBB Genome Research
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Submitted (16-AUG-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 Dases 1 to 164217)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (01-FEB-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Greek, CA 94598, USA On Feb 1, 2002 this sequence version replaced gi:15193398. Draft Sequence Produced by DOE Joint Genome Institute
                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 164217)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Finishing Completed at Stanford Human Genome Center
www-shgc.stanford.dom
Ouality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.1.
Location/Qualifiers
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81.2%; Pred. No. 3.5;
cive 0; Mismatches
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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DOE Joint Genome Institute.
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Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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Submitted (26-JUN-2001) DOB Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 157325)
DOB Joint Genome Institute and Stanford Human Genome Center.
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DOB Joint Genome Institute and Stanford Human Genome Center. Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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DOB Joint Genome Institute and Stanford Human Genome Center.
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Homo sapiens chromosome 5 clone RP11-26302, complete sequence.
AC091264
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Homo sapiens chromosome 5 clone CTD-2096I23, complete sequence.
ACOO8810
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ilarity 81.2%; Pred. No. 3.6;
Conservative 0; Mismatches 9;
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Quality: Phrap Quality >=40 99.7% of Sec
Estimated Total Number of Errors is 0.3.
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/clone="CTD-2096123"
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DOE Joint Genome Institute.
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ROD 29-JUN-2002

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Diract Submission

Submitted (29-JUN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquaries:

Cambridgeshire, CB10 18A, UK. E-mail enquaries:

humquery@sanger ac.uk Clone requests: clonerequest@sanger.ac.uk

On Apr 7, 2002 this sequence version replaced gi:14141369.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one MIS subclone; and the assembly was contirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; WP:, WORMPEP; Information on the WORMPEP; http://www.compared.com/double-strandery/double-strandery/double-strandery/double-strandery/double-strandery/double-strandery/double-strandery/double-strandery/double-strandery/double-strandery/double-strandery/double-strandery/double-strandery/double-strandery/double-strandery/double-strandery/double-strandery/double-strandery/double-strandery/double-strandery/double-strandery/double-strandery/double-strandery/double-strandery/double-strandery/double-strandery/double-strandery/double-strandery/double-strandery/double-strandery/double-strandery/double-strandery/double-strandery/double-strandery/double-strandery/double-strandery/double-strandery/double-strandery/double-strandery/double-strandery/double-stran
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Mouse DNA sequence from clone RP23-392F1 on chromosome 1, complete
sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 173053)
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For further details see http://www.chori.org/bacpac/home.htm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                   DB 9;
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Site: http://mrcseq.har.mrc.ac.uk
                                                                                                             ch 65.5%; Score 33.4; Di
1 Similarity 78.4%; Pred. No. 3.8;
40; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.9%; Score 32.6; DB
80.9%; Pred. No. 6.6;
ive 0; Mismatches
                   'note="low quality region"
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Center: UK Medical Research Council
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://mrcseq.har.mr
Contact: mouseq@har.mrc.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="RP23-392F1"
/clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GI:20068419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 63.9
Best Local Similarity 80.9
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VECTOR: pBACe3.6
                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL365334
AL365334.13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blakey, S
                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
AL365334/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
VERSION
                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
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                                                 ORIGIN
                                                                                                                                                                                                                                                                                                   엄
                                                                                                                                                                                                                                           à
                                                                                                                                                                                  Center: National Yang Ming University Genome Research Center Center
                                                                                                                                                                                                                                                                                                                The PTB1 Chimpanzee BAC library was prepared from DNA isolated from cultured cells established from the blood of a single male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence Quality Assessment:
This entry has been annotated with sequence estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing vector: pUC18; 100% of reads
Sequencing vector: pUC18; 100% of reads
Chemistry: Dye-terminator Big Dye and ET; 100% of reads Assembly
program: Phrap; version 0.990319
Consensus quality: 207,750 bases at least Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="gap containing unresolved di-nucleotide repeats,
*Max-Planck-Institute for Molecular Genetics, Berlin, Germany, *National Institute of Genetics, Mishima, Japan; *National Yang Ming University Genome Research Center, Taipei,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neighboring clones: PTB-152N20(left) and RP43-055A16(right). Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clones may be obtained from Asao Fujiyama and co-workers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and the assembly was confirmed by restriction digest.
                                                                                                                             *RIKEN Genomic Sciences Center, Yokohama, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Pan troglodytes"
/wol_type="genomic DNA"
/db_xref="taxon:9598"
/db_xref="taxon:9598"
/chronosome="22"
/clone="PTB-153E07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                subclone or more than one M13 subclone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16459. ... 16463
/note="low quality region"
43909. .44908
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6277. .46280
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                                                                                                                                                                                                                                                        Web site: http://genome.ym.edu.tw/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (http://www.gsc.riken.go.jp).
VECTOR: pKS145
                                                                                                                                                                     Genome Center
                                                                                                                                                                                                                                                                                         Contact: sequence@ym.edu.tw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .45771
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                                                                                                                                                                                                                          code: YMGC
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Search completed: May 7, 2004, 14:30:58 Job time: 538.003 secs

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Sequence 1069, Ap
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Sequence 11, Appli
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Sequence 35, Appl
Sequence 10, Appl
Sequence 1, Appli
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Sequence 13701, Appli
Sequence 13701, Appl
Sequence 1038, Appl
Sequence 1118, Appl
Sequence 1118, Appl
Sequence 2188, Appl
Sequence 2188, Appl
                                                                               7, 2004, 13:35:03 ; Search time 25.6094 Seconds (without alignments) 1105.159 Million cell updates/sec
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Sequence 1278, Ap
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(/ggn2_6/ptodata/2/ina/5A_COMB.seq:*
): /ggn2_6/ptodata/2/ina/5B_COMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-205-258-15

US-08-587-375-3

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US-09-205-258-52

US-09-205-258-52

US-09-376-594-886

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US-09-376-594-886

US-09-376-594-896

US-09-376-594-896

US-09-38-352-1552

US-09-38-352-1552

US-09-38-352-1552

US-09-38-352-1552

US-09-387-286-3

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US-09-621-976-317

US-08-56-3718-37

US-08-56-3718-3

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US-09-107-532A-1038

US-09-107-532A-1038

US-09-107-532A-1038

US-09-107-532A-1038

US-09-107-532A-1038

US-09-107-532A-1038

US-09-108-328-328-318
                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                    682709 seqs, 277475446 residues
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Maximum Match 99%
Listing first 45 summaries
                                                       - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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Sequence 1, Application US/08545528D

Patent No. 633773

GENERAL INFORMATION:
APPLICANT: Fraser et al.
TITLE OF INVENTION:
TITLE OF INVENTION: Thereof, and Uses Thereof
FILE REPERENCE: P8193P1
CURRENT FILING DATE: 1995-10-19
PRIOR APPLICATION NUMBER: US/08/545,528D
PRIOR APPLICATION NUMBER: US 08/488,018
PRIOR APPLICATION NUMBER: US 08/488,018
PRIOR APPLICATION NUMBER: US 08/473,545
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                       Sequence 2724, Ap
Sequence 3265, Ap
Sequence 1305, Ap
Sequence 29, Appli
Sequence 4, Appli
Sequence 17, Appli
Sequence 15, Appli
Sequence 14, Appli
Sequence 21, Appli
Sequence 2161, Appli
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                                                                                  US-09-800-729-29
US-09-358-383C-4
US-09-358-383C-4
US-09-358-383C-17
US-09-358-383C-17
US-09-734-674-3
US-09-734-674-3
US-09-734-674-3
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US-09-734-67-4
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US-09-734-601C-657
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Patent No. 6525174

GENERAL INFORMATION:
TITLE OF INVENTION: 207 Human Secreted Proteins
FILLE REFREENCE: PZ007P1

CURRENT APPLICATION NUMBER: US/09/205,258

CURRENT PILING DATE: 1998-12-04

EARLIER APPLICATION NUMBER: PCT/US98/11422

EARLIER APPLICATION NUMBER: 60/048,885

EARLIER APPLICATION NUMBER: 60/049,375

EARLIER PILING DATE: 1997-06-06

EARLIER FILING DATE: 1997-06-06

EARLIER FILING DATE: 1997-06-06

EARLIER FILING DATE: 1997-06-06
                                            US-09-543-681A-3265
US-09-134-000C-1305
                                                                                                                                                                                                                                                                                                                                                               US-09-320-721A-3
US-08-961-527-150
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA; ORGANISM: Mycoplasma genitalium
US-08-545-528D-1
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1245
1245
1618
1618
2656
2667
2000
2001
2001
1004
11137
1137
1137
1238
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RESULT 2
US-09-205-258-15
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                                                                                                                                                                                                                                                  Query Match
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BARLIER FILING DATE: 1997-06-06
BARLIER APPLICATION NUMBER: 60/048, 995
BARLIER FILING DATE: 1997-06-06
BARLIER APPLICATION NUMBER: 60/048, 994
BARLIER APPLICATION NUMBER: 60/048, 997
BARLIER PILING DATE: 1997-06-06
BARLIER PILING DATE: 1997-06-06
BARLIER FILING DATE: 1997-06-06
BARLIER PILING DATE: 1997-06-06
BARLIER FILING DATE: 1997-06-06
BARLIER FILING
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Fatent No. 5952485
GENERAL INFORMATION:
APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Song, Wen-Yuang
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Pandarcadero Center, Eighth Floor
CITY: San Francisco
STREET: Two Pandarcadero Center, Eighth Floor
STREET: USA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                   Length 1018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          746 AAATAGATATTGCTCATTAAGGTAAATATTTTTTTGTTGAATGATG 792
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/567,375
FILING DATE: 04-DEC-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/004,645
FILING DATE: 29-SEP-1995
FILING DATE: O7-UN-1995
FILING DATE: US 08/475,891
FILING DATE: US 08/475,891
FILING DATE: US 08/373,375

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
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TYPE: nucleic acid
STRANDEDNESS: single
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 1018
                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-205-258-15
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US-08-567-375-3/c
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3456 Araaaakdaaciriddargiaraarrargiaaarriacdrgiraaararca 3407
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                    1 ACAAAAAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCA 50
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                                                                                                                                                                                                                                                                                       APPLICANT: Ronald, Pamela C.
APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 15
CORRESPONDENCES 15
CORRESPONDENCE ADDRESS:
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STREET: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47.8%; Score 24.4; DB 2; Length 5992; 68.0%; Pred. No. 20; ive 0; Mismatches 16; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="RRK-B"
/note= "Xa21 Kanthomonas spp. disease
resistance gene RRK-B from rice (oryza
sativa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02370-058910US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: join(512..3149, 3993..4393)
CTHER INFORMATION: /product= "RRK-B"
CTHER INFORMATION: /note= "Xa21 Xanth;
CTHER INFORMATION: resistance gene RRI;
US-08-475-891A-3
                                                                                                                                                                                                              Sequence 3, Application US/08475891A Patent No. 5859339 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 52, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5992 base pairs
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Best Local Similarity 68.05
Matches 34; Conservative
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STRANDEDNESS: sing
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US-08-475-891A-3/c
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US-09-205-258-52
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                                                                                                                  1 ACAAAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCA 50
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        Score 24.4; DB 2; Length 3921;
Pred. No. 19;
0; Mismatches 16; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ronal, Pamela C.
APPLICANT: Ronal, Pamela C.
APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Scabo, Veronique
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 27
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 3921;
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MEDIUM TYPE : Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE : Floppy disk
COMPUTER EN FORDER
SOFTWARE : Refeate #1.0, Version #1.30
SOFTWARE : Refeate #1.0, Version #1.30
SOFTWARE : TALON DATA:
RELIGATION NUMBER: US/08/587,680A
FILING DATE: 17-7AN-1995
RAIOR APPLICATION DATA:
RELIGATION DATA:
RELIGATION DATA:
RELIGATION NUMBER: US 08/373,375
FILING DATE: 07-7JN-1995
RELIGATION NUMBER: US 06/004,645
FILING DATE: US-SEP-1995
RELIGATION NUMBER: US 08/567,375
FILING DATE: US-SEP-1995
RELIGATION NUMBER: US 08/567,375
FILING DATE: US-SEP-1995
RELIGATION NUMBER: US 03/070-058940US
TELECOMMUNICATION INFORMATION:
NAME: BASELIAN, Kevin L.
REGISTRATION NUMBER: 033070-058940US
TELECOMMUNICATION INFORMATION:
NAME: REFERENCE/DOCKET NUMBER: 033070-058940US
TELECOMMUNICATION INFORMATION:
THE ENTERNISH CALL OF SERVICE THE SERVICE THE SERVICE TO SERVICE THE SERVICE TO SERVICE THE SERVICE TO SERVICE THE SERVICE TO SERVICE 
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Two Embarcadero Center, Eighth Floor
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68.0%; Pred. No. 19;
ive 0; Mismatches 16;
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; OTHER INFORMATION: /product= "Xa-21"
US-08-587-680A-3
                                                                                                                                                                                                                                                    RESULT 4
US-08-587-680A-3/c
Sequence 3, Application US/08587680A
FRIENT NO. 5977434
GENERAL INFORMATION:
Query Match
Best Local Similarity 68.0%;
Matches 34; Conservative
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 68.0
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 3921 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Two bullers
CITY: San Francisco
STATE: California
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Gaps

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PAPLICANT. YOUNG et al.
TITLE OF INVENTION: 207 Human Secreted Proteins FILE REPRENCE: P2007P1
CURRENT FILE OF INVENTION: 207 Human Secreted Proteins FILE REPRENCE: P2007P1
CURRENT FILE OF STATE STATES PRINCE: P2007P2
CURRENT FILE OF STATES STATES PRINCE OF GENERALIER FILENC DATE: 1997-06-06
EARLIER PELINC DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048 996
EARLIER APPLICATION NUMBER: 60/048 997
EARLIER PILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048 991
EARLIER FILING DATE: 1997-06-06
EARLIER PELING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048 91
EARLIER PERINCEDATION NUMBER: 60/048 91
EARLIER APPLICATION NUMBER: 60/048 91
EARLIER APPLICATIO
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RESULT 8
103-09-976-594-886/c
1 Sequence 886, Application US/09976594
1 Patent No. 6673549
1 GENERAL INFORMATION:
1 APPLICANT: Furness, Michael
1 APPLICANT: Buchbinder, Jenny
2 TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APELICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDE
FILE REPERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR PRIOR PILING DATE: 2000-10-12
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL PROGRAM
SOFTWARE: PEG ID NOS: 1163
SOFTWARE: DEG ID NOS: 1069
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 1011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 1856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 AAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           258 CAAAAAGATAGAGGATTTAAATTTCACAATTGATGTGCTTTAA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 CAAAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6673549 107309.1
NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 24; Pred. No. 2
                                        EARLIER APPLICATION NUMBER: 60/048,67/
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER APPLICATION NUMBER: 100/094,657
                          FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1069, Application US/09976594
Patent No. 6673549
PERERAL INFORMATION:
APPLICANT: Furness, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 47.1%;
1 Similarity 68.8%;
33; Conservative (
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APPLICATION NUMBER:
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Best Local Similarity 72.1
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1011
TYPE: DNA
ORGANISM: Homo sapiens
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Matches 33; Conserv
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OTHER INFORMATION: n equals a, t, c, or NAME/KEY: misc features
LOCATION: (682442)...(682442)
OTHER INFORMATION: n equals a, t, c, or NAME/KEY: misc feature
LOCATION: (713652)...(713652)
OTHER INFORMATION: n equals a, t, c, or OTHER INFORMATION: n equals a, t, c, or or other information: n equals a, t, c, or other information: n equal
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LOCATION: (312837). (312837)
THER INPORMATION: nequals a, t,
NAME/KRY: misc feature
LOCATION: (31293). (31293)
OTHER INPORMATION: nequals a, t,
NAME/KRY: misc feature
LOCATION: (319226). (319226)
OTHER INPORMATION: nequals a, t,
NAME/KRY: misc feature
LOCATION: (559167). (559167)
OTHER INPORMATION: nequals a, t,
NAME/KRY: misc feature
LOCATION: (559241). (559241)
OTHER INPORMATION: nequals a, t,
NAME/KRY: misc feature
LOCATION: (559241). (559241)
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LOCATION: (163385). (163385)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (191989). (191989)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (191995). (191995)
OTHER INFORMATION: n equals a, t,
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LOCATION: (231980). (231980)
OTHER INFORMATION: n equals a, t
NAME/KEY: misc feature
LOCATION: (234187). (234187)
OTHER INFORMATION: n equals a, t
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LOCATION: (600992)..(600992)
OTHER INFORMATION: n equals a, t
NAME/KEY: misc feature
LOCATION: (622708)..(622708)
OTHER INFORMATION: n equals a, t
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LOCATION: (657081)..(657081)
OTHER INFORMATION: n equals a, t
NAME/KEY: misc feature
LOCATION: (657203)..(657203)
OTHER INFORMATION: n equals a, t
NAME/KEX: misc_feature
                                                                                                                                      LOCATION: (103998)..(103998)
OTHER INFORMATION: n equals a,
NAME/KEY: misc. feature
LOCATION: (148948)..(148948)
OTHER INFORMATION: n equals a,
                                        LOCATION: (98343)..(98343)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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LOCATION: (309398)..(309398)
OTHER INFORMATION: n equals a,
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,
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LOCATION: (234220)..(234220)
OTHER INFORMATION: n equals a,
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Fatent No. 6503729

GENERAL INFORMATION:
APPLICAMY: Bult et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ Patent No. 6503729

TITLE OF INVENTION: jannaschii
FILE REFERENCE: PB275

TITLE OF INVENTION: jannaschii
FILE REFERENCE: PB275

CURRENT APPLICATION NUMBER: US/08/916,421B

CURRENT FILING DATE: 1997-08-22

FRIOR APPLICATION NUMBER: US 60/024,428

FRIOR APPLICATION NUMBER: US 60/024,428

FRIOR APPLICATION NUMBER: US 60/024,428

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PATENTIN VETSION 3.1
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Pred. No. 27;
0; Mismatches 7; Indels 0
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; NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6673549 981037.1
US-09-976-594-886
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FILE REFERENCE: PA-0041 US
CURRENT PEPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR PLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL Program
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LOCATION: (98120). (98120)
OTHER INFORMATION: nequals a, t, c,
NAME/KEY: misc feature
LOCATION: (98159). (98159)
OTHER INFORMATION: nequals a, t, c,
NAME/KEY: misc feature
LOCATION: (98239). (98239)
OTHER INFORMATION: nequals a, t, c,
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LENGTH: 1664976
TYPE: DNA
ORGANISM: Methanococcus jannaschii
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LOCATION: (98266)..(98266)
OTHER INFORMATION: n equals a, t,
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NAME/KEY: misc_feature
LOCATION: (28222). (28222)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals a, t.
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LOCATION: (84773)..(84773)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (84808)..(84808)
OTHER INFORMATION: n equals a, t
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OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 80.0%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                LENGTH: 1312
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US-08-916-421B-1
                                                                                                                                                                                                                              SEQ ID NO 886
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APPLICANT: Buchbinder, Jenny
TILB OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDE
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594

CURRENT FILING DATE: 2001-10-12

PRIOR PRILING DATE: 2000-10-12

NUMBER OF SEQ ID NOS: 1143

SOFTWARE: PERL PROGRAM

SEQ ID NO 690

LENGTH: 6609
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ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
THERROF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5196 ACCAAAATAAATTGTGAAAAAGATAAAGACTTTCATCTTCAAACAAC 5148
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                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
CHER INFORMATION: Incyte ID No. 6673549 175918.15
NAME/KEY: unsure
LOCATION: 825
COTHER INFORMATION: a, t, c, g, or other
US-09-976-594-690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     658324 TGAAACTTAAAACTTTTGTGCCTCAAAAAAA 658292
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45.9%; Score 23.4; D
Best Local Similarity 67.3%; Pred. No. 43;
Matches 33; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
US-09-751-389-3/C
; Sequence 3, Application US/09751389
; Patent No. 6630334
; GENERAL INFORMATION:
    APPLICANT: GUEGLER, Karl et al
    TITLE OF INVENTION: ISOLATED HUMAN KINASE PRO
    TITLE OF INVENTION: THEREOF
    TITLE OF INVENTION: ACID MOLECULES ENCODING
    TITLE OF INVENTION: 2001067
    CURRENT APPLICATION NUMBER: US/09/751,389
    CURRENT FILING DATE: 2001-01-02
    NUMBER OF SEQ ID NOS: 8
    SOFWWARE: Fastes of for Windows Version 4.0
    SEQ ID NO 3
    LENGTH: 786431
    TYPE: DNA
    CREANISM: Human
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81.8%; Pred. No. 65;
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LOCATION: (1)...(786431)
OTHER INFORMATION: n = A,T,C or G
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Matches 27; Conservative
                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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1 Similarity 66.7%; Pred. No. 50;
34; Conservative 0; Mismatches
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                                  NAME/KEY: misc feature
LOCATION: (779455)...(779455)
OTHER INFORMATION: n equals a, t, c,
NAME/KEY: misc feature
LOCATION: (779676)...(779676)
OTHER INFORMATION: n equals a, t, c,
NAME/KEY: misc feature
LOCATION: (855539)...(855539)
OTHER INFORMATION: n equals a, t, c,
NAME/KEY: misc feature
LOCATION: (875539)...(85539)
OTHER INFORMATION: n equals a, t, c,
NAME/KEY: misc feature
LOCATION: (871619).
OTHER INFORMATION: n equals a, t, c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (1637998). (1637998)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (1664854). (1664855)
OTHER INFORMATION: n equals a, t,
  LOCATION: (741684)..(741684)
OTHER INFORMATION: n equals a, t,
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OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (1559020)...(1569020)
OTHER INFORMATION: n equals a, t,
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LOCATION: (1310988). (1310988)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (1313224). (1313224)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (1349473). (1349473)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (1349491). (1349491)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
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LOCATION: (1084830)..(1084830)
OTHER INFORMATION: n equals a,
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LOCATION: (1096846)..(1096846)
OTHER INFORMATION: n equals a,
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LOCATION: (1130881).
OTHER INFORMATION: n equals a,
NAME/KEY: misc_feature
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LOCATION: (1603734)..(1603734)
OTHER INFORMATION: n equals a,
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LOCATION: (1119881)..(1119881)
OTHER INFORMATION: n equals a,
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Best Local Similarity
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US-08-916-421B-1
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Sequence 1552, Application US/09328352
Patent No. 6562958
Patent No. 6562958
TITLE OF INVENTION: Breton et al.
TITLE OF INVENTION: BUCHERC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILL REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352

US-09-328-352-1552

Sequence 690, Application US/09976594; Patent No. 6673549; GENERAL INFORMATION:

RESULT 10 US-09-976-594-690/c

g

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APPLICANT: Lagace, Robert, E.
APPLICANT: Patterson, Chandra
APPLICANT: Berg, Kim, L.
TITLE OF INVENTION: NUCLECTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
FILE REFERENCE: PM-0008-4 US
CURRENT APPLICATION NUMBER: US/09/596,002
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: 60/140,121
PRIOR FILING DATE: 1999-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1287 AATCCAAAAAGCCTTTAATTTTAATTTCTTTGTTGCATAAATATCA 1241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.1%; Score 23; DB 4; Length 19988; 68.1%; Pred. No. 65; tive 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 AAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
OTHER INFORMATION: Incyte template ID No. 6632636 10
; PUBLICATION INFORMATION:
US-09-596-002-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7, 2004, 15:44:33
                                                                                                Sequence 10, Application US/09596002
Patent No. 6632636
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
SOFTWARE: PERL Program
SEQ ID NO 10
LENGTH: 19988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 68.1<sup>§</sup>
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: M. catarrhalis
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: May 'Job time: 34.6094 secs
                                                                             JS-09-596-002-10/c
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US-09-540-236-1082/c

US-09-540-236-1082/c

Sequence 1082, Application US/09540236

FREEDI NO. 6673910

GENERAL INFORMATION:

APPLICANT: GATY L. Breton et al.

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709-2005-001

CURRENT APPLICATION NUMBER: US/09/540,236

CURRENT FILING DATE: 2000-04-04

NUMBER OF SEQ ID NOS: 3840

SEQ ID NO 1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INCROMATION:

APPLICANT: Lynn Dougette-Stamm et al

TITLE OF INVENTION:

TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1999-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 1278
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                                                                                                                                                                                     DB 4; Length 963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      394 AArccaaaaagcrrraaarrraarrrcrrrcrrgcaraaararca 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.1%; Score 23; DB 4; Length 1026; 68.1%; Pred. No. 49; tive 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                  263 ATATTAATGAAGTGGACTTAAATGTACGTCCTTTTGTTCTTAAA 306
                                                                                                                                                                                                                             13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 AAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1360 CAAAAAGAAACTGGTATTAAAGGTAAACAATTATT 1395
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                                                                                                                                                                                   Score 23.2; D
Pred. No. 42;
0; Mismatches
                                                                                                                                                                                                                                                                        1 ACAAAAAGAAATTGGACTTAAAGTTAAATACTT
                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
2-09-134-001C-1278
Sequence 1278, Application US/09134001C
Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Staphylococcus epidermidis
                                                                                         ; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-1552
CURRENT FILING DATE: 1999-06-04 UNDBER OF SEQ ID NOS: 8252 LENGTH: 963
                                                                                                                                                                                   45.5%;
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Best Local Similarity 68.1
Matches 32; Conservative
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Best Local Similarity
Matches 31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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Gaps

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5.1.6
Compugen Ltd.
GenCore version (c) 1993 - 2004
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- nucleic search, using sw model OM nucleic

Run on:

7, 2004, 11:56:28; Search time 104.189 Seconds (without alignments) 2079.475 Million cell updates/sec

US-10-071-411A-1_COPY_450_500 Perfect score: Title:

1 acaaaaagaaattggactta......ttttgtgcttcaaacatcat Sequence:

Gapop 10.0 , Gapext 1.0

IDENTITY NUC

Scoring table:

Searched:

Total number of hits satisfying chosen parameters:

3373863 seqs, 2124099041 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Maximum Match 99% Listing first 45 summaries Post-processing: Minimum Match 0%

N_Geneseq_29Jan04:* Database :

geneseqn2001as:* geneseqn2001bs:* geneseqn2003as:* geneseqn2003ba:* geneseqn2003cs:* geneseqn1980s:* geneseqn1990s:* geneseqn2000s:* geneseqn2004s:* geneseqn2002s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

		oh			SUMMARIES	
Result No.	. Score	Query Match	Query Match Length DB	DB	ID	Description
; '1' ! !		94.1	168174	9	ABT11173	Abt11173 Human 5-1
• •	2 48	94.1	168273	9	ABT11114	Human
**1	3 38.4	75.3	13249	9	ABL32116	Human
υ	4 38.4	75.3	13249	9	ABL32117	Human
U	38.4	75.3	13249	9	ABK31177	Signal
•		75.3	13249	9	ABK31176	Abk31176 Signal tr
υ	7 38.4	75.3	13249	9	ABL70132	
~	38.4	75.3	13249	9	ABL70131	_
υ	7	56.1	879	7	ACA39547	
c 10	7	56.1	10809	7	ACC69139	
1		56.1	80073	~	AAT58840 5	Continuation (6 of
1;	2 28.6	56.1	110000	~	AAT58840 4	2
C T		51.8	355	4	AAI83146	, H
-	4 25.6	50.2	5864	ø	ABL33441	
0		50.2	5864	ø	ABL54362	Chemi
ŭ	N	50.2	349938	σ	ADC87621	
H	7 25.4	49.8	607	Ŋ	ABV58521	
ĩ	25.	49.4	206	4	AAK81112	
_	9 25.2	49.4		e	AAZ93368	Aaz93368 Sequence
N	0 25.2	49.4	1214	ø	AAL41059	Aal41059 cDNA of H
N	1 25.2	49.4	1285	4	ABK41870	Abk41870 cDNA enco
0		49.4	1285	ω	ADB59537	Conne
2	3 25.2	49.4	1779	٣	AAC80574	Aac80574 Human sec

Aak81109 Human imm Aak81111 Human imm	,	Abl17308 Drosophil		Continuation (2 of	Acd13446 Human DNA	Aai81019 Human pol		Aav84415 Human sec	Aba83198 Human sec	Ach04699 Novel hum	Acd44509 Human cDN	Abk73006 Bacillus	Aak78949 Human imm	Aad48267 Ehrlichia	Abl33138 Human imm	Aal04782 Human rep	Abl97677 Human tes	Ada02576 Human FKB	Adb72314 Human FKB
AAK81109 AAK81111	AAK81110	ABL17308	ABL33240	AAL52246 1	ACD13446_	AAI81019	ABK72766	AAV84415	ABA83198	ACH04699	ACD44509	ABK73006	AAK78949	AAD48267	ABL33138	AAL04782	ABL97677	ADA02576	ADB72314
4 4	4, 4	4	9	7	7	4	9	N	4	œ	80	9	4	9	ø	4	4	œ	σ
5728	5733	4129	9888	110000	240000	446	948	1018	1018	1018	1018	1218	3982	4460	5678	22927	22927	87878	87878
4.4.	49.4	49.0	49.0	49.0	0.	48.2	.2	.2	48.2	48.2	48.2	48.2	.2	.2		.2		.2	
4 6 9	4 4	4	4	4	49.0	4	48.2	48	4.5	4 8	4	4.6	4	48	4	48	48	48	48
25.2	25.2	25	25	25	25	24.6	24.6	24.6	24.6	24.6	24.6	24.6	24.6	24.6	24.6	24.6	24.6	24.6	24.6
24	26	8	53	30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	45
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ALIGNMENTS

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Human; polymorphic region; 5-lipoxygenase; 5-LO gene; asthma; bronchitis; sinusitis; ulcerative colitis; nephritis; amyloidosis; sarcoidosis; rheumatoid arthritis; scleroderma; lupus; non-allergic rhinitis; polymyositis; Reiter's syndrome; psoriasis; pelvic inflammatory disease; atopic; contact dermatitis; forensic medicine; paternity testing; enzyme;
                                                                      Human 5-lipoxygenase gene related DNA sequence SEQ ID No 63.
                  ABT11173 standard; DNA; 168174 BP.
                                                    (first entry)
                                                    05-DEC-2002
                                    ABT11173;
RESULT 1
          ABT111
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07-FEB-2002; 2002WO-US003546. WO200262825-A2. Homo sapiens. 15-AUG-2002.

08-FEB-2001; 2001US-0267515P. 21-AUG-2001; 2001US-0314248P.

(MILL-) MILLENNIUM PHARM INC.

Meyer J; Barnes G, WPI; 2002-627522/67.

New isolated nucleic acid molecule with an allelic variant of a belymorphic region of an 5-LO gene, useful for diagnosing and/or prognosticating disorders associated with an aberrant inflammatory response such as asthma

Disclosure, Fig 4; 290pp; English.

The invention relates to an isolated human nucleic acid molecule comprising an allelic variant of a polymorphic region of a 5-lipoxygenase (5-L0) gene, where the allelic variant comprises one or more nuclectide selected from any of 3, 20 or 21 base pair sequences, given in the specification, or their complement. The compositions and methods of the

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associated with an aberrant inflammatory response such as asthma, bronchitis, sinusitis, ulcerative colitis, nephritis, amyloidosis, rheumatorid arthritis, sarcoidosis, scleroderma, lupus, non-allergic rhinitis, polymyositis, Reiter's syndrome, psoriasis, polymyositis, Reiter's syndrome, psoriasis, polymic inflammatory disease, atopic and contact dermatitis. The nucleic acid molecules can also be useful for identifying an individual amongst other individuals from the same species for use in forensic medicine and paternity testing. This polymucleotide sequence represents DNA relating to the human 5-lipoxygenase (5-LO) gene of the invention
      for diagnosing and/or prognosing disorders
invention are useful
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Sequence 168174 BP; 46808 A; 36442 C; 36942 G; 46474 T; 0 U; 1508 Other;

ö Gaps o; Length 168174; 0; Indels 94.1%; Score 48; DB 6; Le 100.0%; Pred. No. 8.9e-06; iive 0; Mismatches 0; Conservative Query Match Best Local Similarity 48; Matches

166822 AAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT 166869 51 4 AAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT d à

RESULT 2 ABT11114

ABT11114 standard; DNA; 168273

(first entry) 05-DEC-2002

ABT11114;

Human 5-lipoxygenase gene related DNA sequence SEQ ID No 2.

Human; polymorphic region; 5-lipoxygenase; 5-LO gene; asthma; bronchitis; sinusitis; ulcerative colltis; nephritis; amyloidosis; sarcoidosis; rheumatoid arthritis; scleroderma; lupus; non-allergic rhinitis; polymyositis; Reiter's syndrome; psoriasis; pelvic inflammatory disease; atopic; contact dermatitis; forensic medicine; paternity testing; enzyme;

Homo sapiens.

WO200262825-A2.

15-AUG-2002,

07-FEB-2002; 2002WO-US003546.

08-FEB-2001; 2001US-0267515P. 21-AUG-2001; 2001US-0314248P.

(MILL-) MILLENNIUM PHARM INC.

Meyer J; D, Barnes WPI; 2002-627522/67.

New isolated nucleic acid molecule with an allelic variant of a polymorphic region of an 5-LO gene, useful for diagnosing and/or prognosticating disorders associated with an aberrant inflammatory response such as asthma.

Disclosure; Fig 2; 290pp; English.

The invention relates to an isolated human nucleic acid molecule comprising an allelic variant of a polymorphic region of a 5-lipoxygenase (5-LO) gene, where the allelic variant comprises one or more nucleotide selected from any of 3, 20 or 21 base pair sequences, given in the specification, or their complement. The compositions and methods of the present invention are useful for diagnosing and/or prognosing disorders associated with an aberrant inflammatory response such as asthma, bronchitis, sinusitis, ulcerative colitis, nephritis, amyloidosis, rheumatoid arthritis, sarcoidosis, scleroderma, lupus, non-allergic rhinitis, polymyositis, Reiter's syndrome, psoriasis, pelvic inflammatory

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Gaps

· 0

Indels

9

0; Mismatches

6; Length 13249;

Score 38.4; DB 6; Pred. No. 0.0082;

75.3%; 87.5%;

Best Local Similarity 87.5 Matches 42; Conservative

Query Match

Sequence 13249 BP; 3594 A; 273 C; 3130 G; 6252 T; 0 U; 0 Other;

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0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system discorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AnDs, epilepsy, neurofibromatosis, rheumatoid archritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                  also be useful for identifying an individual amongst other individuals from the same species for use in forensic medicine and paternity testing. This polynuclectide sequence represents DNA relating to the human 5-lipoxygenase (5-LO) gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirhemmatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for
                                                                                                     Sequence 168273 BP; 46834 A; 36467 C; 36966 G; 46498 T; 0 U; 1508 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid comprising fragment of chemically modified gene, useful diagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                                                                                              Gaps
 contact dermatitis. The nucleic acid molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                             166921 AAAAGAAATIGGACITAAAGITAAATACITTTGIGCTICAAACAICAT 166968
                                                                                                                                                                              0;
                                                                                                                                           Length 168273;
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                                                                                                                                                                                                             AAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT
                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immune system associated gene SEQ ID NO: 89.
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hes 0;
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                                                                                                                             94.1%; Scor.
100.0%; Pred. No. o...
... 0; Mismatches
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01-SEP-2000; 2000DE-01043826.
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                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                            Conservative
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   disease, atopic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-130909/17
                                                                                                                                    Query Match
Best Local Similarity
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The present invention relates to chemically modified DNA sequences of signal transduction associated genes. The DNA sequences are chemically modified using a solution of bisulphite, hydrogen sulphite of also disclosed are oligonuclectides and/or PNA oligomers for detecting the cytosine methylation state (CpG islands) of these genes, and a method for the cytosine methylation state (CpG islands) of these genes, and a method correlated with signal transduction. The genomic DNA can be contained from cells or cellular components which contain DNA, e.g. cell lines, biopsise, blood, sputum, stool, urine, cerebral-spinal fluid, tissue embedded in paraffin such as tissue from eyes, intestine, kidney, brain, heart, prostate, lung, breast or liver, histologic object slides, cand all their possible combinations. The sequences of the invention are useful for the diagnosis and therapy of diseases associated with signal transduction e.g. solid tumours and cancer. ABK31158-ABK31545 represent commissionally preterated genomic DNA sequences of different genes associated with signal transduction, or their complementary sequences. Note: The sequence data for this patent did not form part of the printed
                                                                                                                Human, signal transduction associated gene, cytosine methylation state, CpG island, signal transduction associated disease, solid tumour, cancer, antitumour, cytostatic, mutant, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic sequences of genes associated with signal transduction.
                                                                Signal transduction associated gene modified complementary DNA #10.
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larity 87.5%; Pred. No. 0.0082;
Conservative 0; Mismatches 6; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 20; 24pp; English.
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01-SEP-2000; 2000DE-01043826.
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                                                                                                                                                                                                                                                                                                                                                                            29-JUN-2001; 2001WO-EP007472.
                   (first entry)
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                      23-APR-2002
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Matches
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AC ABK3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system discorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, Alzheitys, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                    Human; immune system disease; cytosine methylation; antiasthmatic; antiartiscilerotic; antianaemic; cytostatic; nototropic; antianaemic; anticomvulsant; ophthalmologic; anticherotic; anticomvulsant; ophthalmologic; anticheromatic; antiarthritic; antidiabetic; antipsoriatic; antininflammatory; cancer; eye disease; arterisosterosis; ansemia; antiantiale myeloid leukaemia; Altheimer's disease; AlDS; epilepsy; acute myeloid seukaemia; altheimer's disease; AlDS; epilepsy; antiantialibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation.
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            4 AAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT
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                                                                                                                                                                                                                                                                                                                          system associated gene SEQ ID NO: 90.
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01-SEP-2000; 2000DE-01043826
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Best Local Similarity
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ABK31177/c
ID ABK3117
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The present invention relates to chemically modified DNA sequences of signal transduction associated genes. The DNA sequences are chemically modified using a solution of bisulphite, hydrogen sulphite or disulphite.

Also disclosed are oligomucleotides and/or PNA oligomers for detecting the cytosine methylation state (CpG islands) of these genes, and a method for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with signal transduction. The genomic DNA can be obtained from cells or cellular components which contain DNA, e.g. cell innes, biopsies, blood, sputum, stool, urine, cerebral-spinal fluid, tissue embedded in paraffin such as tissue from eyes, intestine, kidney, brain, heart, prostate, lung, breast or liver, histologic object slides, cuseful for the diagnosis and therapy of diseases associated with signal transduction e.g. solid tumours and cancer. ABK31158-ABK31545 represent commission, or their complementary sequences. Note: The sequence data for this patent did not form part of the printed complementary sequences. Note: The received the printed complementary sequences. Note: The received by the signal transduction, or their complementary sequences. Note: The received by the printed complementary sequences. Note: The received by the printed complementary sequences. Note: The received by the printed complementary sequences.
                   Human, signal transduction associated gene; cytosine methylation state; CpG island; signal transduction associated disease; solid tumour; cancer; antitumour; cytostatic; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligonucleotide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic sequences of genes associated with signal transduction.
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01-SEP-2000; 2000DE-01043826.
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                                                                                                                                                                                                                                                                                                                                                                                                 (EPIG-) EPIGENOMICS AG.
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                                                                                                                                                                                 WO200200926-A2.
                                                                                                                 sapiens
                                                                                                                                                                                                                                   03-JAN-2002
                                                                                                                                       Synthetic
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0; Gaps ·. Score 38.4; DB 6; Length 13249; Pred. No. 0.0082; 0; Mismatches 6; Indels 0; 4 AAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT 6; Indels 75.3%; ilarity 87.5%; Conservative (Local Similarity nes 42; Conserv Query Match Matches à

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ABL70132 standard; DNA; 13249 BP 01-JUL-2002 ABL70132;

(first entry)

Chemically treated cell signalling DNA sequence complementary to#11.

Cell signalling; cytosine methylation; cell signalling disease; cancer; tumour; cytostatic; ds.

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The invention relates to a nucleic acid comprising a sequence of at least labbases of a segment of chemically pretreated DNA of genes associated with cell signaling. The activity of the modified sequences of the invention may be described as cytostatic. The object of the invention is to provide the chemically modified DNA of genes associated with cell signalling, as well as an method which is particularly suitable for the diagnosis and/or PNA-oligomers for particularly suitable for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with cell signalling. The chemically modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as solid tumours and cancer. The sequences given in records ABL70111-ABL70626 represent chemically pre-treated genomic DNA's of genes associated with cell signalling. Note: The sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                             Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signaling e.g. cancer, comprises chemically modified genomic sequences of genes associated with cell signaling.
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0; Mismatches 6;
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Piepenbrock C,

olek A,

(EPIG-) EPIGENOMICS

29-JUN-2001; 2001WO-EP007471 30-JUN-2000; 2000DE-01032529 01-SEP-2000; 2000DE-01043826

WO200202807-A2

10-JAN-2002

Unidentified

51 4 AAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT

셤

ABL70131 standard; DNA; 13249 01-JUL-2002 (first entry) RESULT 8 #X#X#X#XXXXXXXXXXX

Chemically treated cell signalling DNA sequence#11.

signalling; cytosine methylation; cell signalling disease; cancer; cumour; cytostatic; ds.

Unidentified.

WO200202807-A2

10-JAN-2002

29-JUN-2001; 2001WO-EP007471.

30-JUN-2000; 2000DE-01032529.

2003-029926/02

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The invention relates to a nucleic acid comprising a sequence of at least 18 bases of a segment of chemically pretreated DNA of genes associated with cell signaling. The activity of the modified sequences of the invention may be described as cytostatic. The object of the invention is signalling, as well as oligonucleotides and/or PNA-oligomers for detecting cytosine methylations, as well as a method which is particularly suitable for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with cell signalling. The chemically modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as sociated with cell signalling. The chemically modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as sociated with cell signalling. Note: The sequence data for this patent is not represented in the printed sequence data for this patent is not represented in the printed process and the continuous pates.
                                                                                                                                                                            Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signaling e.g. cancer, comprises chemically modified genomic sequences of genes associated with cell signaling.
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                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 21; 24pp + Sequence Listing; English
                                                                                          Berlin K;
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  01-SEP-2000; 2000DE-01043826.
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87.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 87.5
les 42; Conservative
                                                                                          Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Buropean Patent Office
                                             (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycoplasma genitalium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          drug design; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACA39547;
                                                                                          Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
ਨੇ
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·, Gaps 0; 6; Length 13249; 21 Score 38.4; DB 6; Lengtn L. Pred. No. 0.0082; 4 AAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT 0; Mismatches

WO200277183-A2. 03-OCT-2002.

21-MAR-2001; 2001US-00815242. 06-SEP-2001; 2001US-00948993. 25-0CT-2001; 2001US-0342923P. 08-FEB-2002; 2002US-00072851. 21-MAR-2002; 2002WO-US009107

(ELIT-) ELITRA PHARM INC.

06-MAR-2002; 2002US-0362699P

Ohlsen KL, Forsyth RA, Haselbeck R, Yamamoto R, Malone C, Carr GJ, Zamudio C, Trawick JD, Wang L, Wall D,

Zyskind JW; Xu HH;

the inventory legace to an instruction and the care compression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a promoter operably linked to the nucleic acid encoding a promoter operably linked to the nucleic acid encoding a proposesion is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated of polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular to proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway contained for proliferation, (7) identifying a compound that influences the activity of the gene product of the gene product of the gene product lies of an agene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound sactivity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent of which each of the strains is present in a culture or collection of strains; or (13) identifying proteins or screening for homologous nucleic acids are useful for cidentifying proteins or for screening for mandider models and acids required for callular proliferation of an organism. The antisense models are useful for dentifying proteins or for screening for homologous nucleic acids required for or for screening for promoted acids required for callular proliferation of an organism. The acid and identifying acids are useful for compound and acids are useful for contained and acids are useful for contains and acids are useful for contains and acids are useful for contains or for screening the processing and acids are useful for contains and acids are useful for contains and acids are useful for contains and acid New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs. drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at Gaps The invention relates to an isolated nucleic acid comprising any 537 ACTAAAAGGATTTGGAATGAAAGTAGAATACTTTTTCCTTTAACAGTAAT 487 ; 1 ACAAAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT 51 DB 7; Length 879; Sequence 879 BP; 269 A; 120 C; 143 G; 347 T; 0 U; 0 Other; 14; Indels 56.1%; Score 28.6; DE 72.5%; Pred. No. 8.8; cive 0; Mismatches Claim 14; SEQ ID NO 27417; 1766pp; English. electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences ACC69139 standard; DNA; 10809 37; Conservative Local Similarity Query Match Matches RESULT 10 ACC69139/ 8 g

(first entry) 10-JUL-2003 ACC69139;

.; 0

Mycoplasma genitalium; gene cassette; replication; transcription; translation; metabolism; basic genetic operating system; gene therapy; autonomous protecrophic nanomachine; auxotrophic nanomachine; nanomachine; bioreactor; bioreamediation; therapeutic; delivery system; artificial tissue; artificial organ system; energy conversion system; processing system; anabolic system; catabolic system; biological film; M. genitalium aerobic metabolism gene cassette DNA SEQ ID NO:7. coating; cosmetic; gene; ds. biological

Mycoplasma genitalium

. 0

Gaps

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Indels

DB 2; Length 110000;

Score 28.6; DE Pred. No. 12; 0; Mismatches

0;

ВР

210000 310000 410000 510000

110000

57

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of 6) of AAT58840 from base 400001 (Mycoplasma genitalium genome.
It into 6 fragments LOCUS AAT58840 Accession Aat58840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to human polymucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymerides are useful in gene therapy, vaccines or e.g. stem cell growth factor activity, nematopoiesis regulating activity, issue growth factor activity, immunomodulatory activity and activity, issue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunocallatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                  1 ACAAAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 3206; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human polynucleotide SEQ ID NO 3206.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-FEB-2001; 2001WO-US004927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAI83146 standard; cDNA; 355
                                                                                                                                                                                                                                                56.1%;
                                                                                                                                                                       300001
400001
500001
                                                                                                                                  100001
                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001-514838/56.
                                                                                                                                                                                                                                                                      Similarity
37; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAO03215
                                                                                           Fragment Name
AAT58840 0
AAT58840 1
AAT58840 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                     AAT58840 3
AAT58840 4
AAT58840 5
                                                                         Sequence split
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-NOV-2001
                                                Continuation (5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAI83146;
                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAI83146/c
                                                                                                                                                                                                                                                                          Best Loc
Matches
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                                    AAT58840
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Continuation (6 of 6) of AAT58840 from base 500001 (Mycoplasma genitalium genome.)
WP Sequence split into 6 fragments LOCUS AAT58840 Accession Aat58840
WP AAT58840 1 10000
WP AAT58840 2 200001 310000
WP AAT58840 3 300001 410000
WP AAT58840 400001 510000
WP AAT58840 5 500001 50000
                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a basic genetic operating system for an autonomous prototrophic or auxotrophic nanomachine comprising a nanomachine genome encoding a minimal gene set sufficient for viability or replication, optionally in the presence of an auxotrophic molecule.

Also described is an autonomus prototrophic or auxotrophic nanomachine comprising a basic genetic operating system for autoromous prototrophic or auxotrophic molecule, and a particle envelope. The nanomachines can be used in gene therapy. The basic genetic operating system or nanomachine is used in gene therapy. The basic genetic operating system or nanomachine is used in therapeutic, diagnostic and industrial applications, e.g. as a bioreactor, for bioremediation, for the production of a therapeutic biomolecule or as a therapeutic reagent, for the production of a therapeutic capacity indicator or reagent, as a delivery system, as an artificial tissue or organ system, as an energy conversion system, as a processing system, as an anabolic or catabolic system, for the production of system, as an anabolic or catabolic system, for the production of sequence represents a Mycoplasma genitalium gene cassette nucleotide sequence, which is used in an example from the present invention for the design and synthesis of a basic genetic operation system for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
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                                                                                                                                                                                                                                                                      New basic genetic operating system for autonomous prototrophic or auxotrophic nanomachine, useful for therapeutic, diagnostic or industrial purposes, comprises a nanomachine genome encoding a gene set for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8476 ACTAAAAGGATTTGGAATGAAAGTAGAATACTTTTTTCCTTTAACAGTAAT 8526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4241 ACTAAAAGGATTTGGAATGAAGTAGAATACTTTTTTTCCTTTAACAGTAAT 4191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10809 BP; 3805 A; 1468 C; 1932 G; 3604 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ACAAAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ACAAAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCAT 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 28.6; DB
Pred. No. 12;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.1%; Score 28.6; DE 72.5%; Pred. No. 10; Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 210-213; 250pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   replication competent nanomachine
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72.5%;
                                                                             18-SEP-2002; 2002WO-US029811
                                                                                                                  20-SEP-2001; 2001US-00960870
                                                                                                                                                        (EGEA-) EGEA BIOSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 72.5
Marches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37; Conservative
                                                                                                                                                                                                                                                                                                                                 viability or replication.
                                                                                                                                                                                                                                  WPI; 2003-354602/33
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WO2003025145-A2
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Best Local 9
                                                                                                                                                                                             Evans GA;
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  8X8X#X#X#X#X#X######X8XX8888#X#X#X#X#X
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Apoptosis; HIV; Bloom syndrome; cardiopathy; neurodegenerative disorder; Herpes simplex virus; renal ischaemia; amyotrophic lateral sclerosis;

06-APR-2001; 2001WO-EP003969.

WO200177164-A2

18-OCT-2001

Unidentified

cancer; ds

2000DE-01019173. 2000DE-01032529. 2000DE-01043826. 2000DE-01019058

30-JUN-2000;

07-APR-2000; 06-APR-2000;

Chemically treated apoptosis gene complementary to gene #31.

(first entry)

29-JUL-2002

ABL54362;

ABL54362 standard; DNA; 5864 BP

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RESULT 15
ABL54362/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirhematic; antiartitic; antidabetic; antipsoriatic; antiinflammatcry; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid comprising fragment of chemically modified gene, useful f
diagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immune system disease; cytosine methylation; antiasthmatic;
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                                                Length 355;
                                                                                                                                                                                           209 ATAAATTGGACTTAAAATTCAAAACTCTTGCCCTTTAAAAGACA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 1414; 32pp + Sequence Listing; German.
                                                                                               11; Indels
                                                                                                                                             7 AGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACATCA 50
Sequence 355 BP; 86 A; 65 C; 74 G; 130 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immune system associated gene SEQ ID NO: 1414.
                                                DB 4;
                                           Score 26.4; DB
Pred. No. 41;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-JUL-2001; 2001WO-EP007537.
                                              Query Match
Best Local Similarity 75.0%;
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                RESULT 14
ABL33441/C
1D ABL33
XX
ABL33441/C
XX
ABL33
XX
DT 26-MA
DT 30-UF
DN WPI;
XX
DN WPI;
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CC GPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                          Chemically modified sequences of genes associated with apoptosis are useful to determine methylation patterns of genomic DNA samples for diagnosis of associated diseases such as cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 6; Length 5864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 50.2%; Score 25.6; D
1 Similarity 70.8%; Pred. No. 89;
34; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7, 2004, 13:50:20
                                                                                                                                                                                                                                                                                                                                Claim 1; Seq ID #62; 24pp; English.
                                                                 Berlin K;
                                                                 Piepenbrock C,
(EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   European patent office
                                                                                                                                  WPI; 2002-017444/02
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Best Local Similarity
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                                                                 olek A,
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Gaps

0;

Length 5864;

Score 25.6; DB 6; Length 5 Pred. No. 89; 0; Mismatches 14; Indels

Query Match
Best Local Similarity 70.8%;
Matches 34; Conservative

1 ACAAAAAGAAATTGGACTTAAAGTTAAATACTTTTGTGCTTCAAACAT 48

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מווו זורכא ווועשווו:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Human DN	AC011879 Homo sapi	ACULUB67 HOMO SADI AX344172 Semience	AX344173 Sequence	AX345018 Sequence	AX345019 Sequence	AX348563 Sequence	ALS90439 Human DNA	AC025758 Homo sapi	AC008810 Homo sapi	ACU33284 NOWO SAPI BS000239 Pan trool	AL365334 Mouse DNA	AL133492 Homo sapi	HOME	Ношо	Pan	HOH	HOM	Homo	Homo	HOM	Homo	Homo	Homo	HOMC	Homo	Hume	HOMO		Homo	Human	(ycopla	tion (6	30698 Homo s	TION (linear	2 on chromosome 10, complete				ertebrata; E	Hominidae; Homo.	
SUMMARIES	AL73156	AC01187	AX34417	AX34417	AX34501	AX34501	AX34856 AX34856	AL59043	AC02575		BS00023	0 AL3653	HS101D0	AC01228	HS21C10	AC14599	AC00497	AC10369	AF23510	ACLOOBI	AC10873	AC01835	AC09977	AC00906	AL35997	AC07424		ACU/332	AC08786	AC02633	CNSOLDW	U39722	AR30019	AC090698	AK3001 AC0158	ALIGNMENTS		129266 bp DNA	clone RP11-		7524		Chordata; Craniata; V	Primates; Catarrh 66)	
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Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Norman, C. H., O'Connor, T., O'Connor, T., O'Connor, T., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, R., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Phyman, D., Ye, W.J., Zimmer, A. and Zody, M., Mheeler, J., Wu, X., Direct Submission
                                                                                                                                                                                                                                                                                                           Submitted (15-007-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON Mar 14, 2000 this sequence version replaced gi:6524208.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center clone name: 16 P 14
Sequencing vector: M13, M78815, 10% of reads
Sequencing vector: M13, M78815, 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 111055 bases at least Q40
Consensus quality: 115056 bases at least Q30
Consensus quality: 147921 bases at least Q20
Insert size: 163000; agarose-fp
Insert size: 157754; sum-of-contigs
Quality coverage: 2.9 in Q20 bases; sum-of-contigs
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gap of 100 bp
contig of 1509 bp in length
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contig of 1209 bp in length
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contig of 1551 bp in length
gap of 100 bp
contig of 1354 bp in length
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contig of 143 bp in length
contig of 143 bp in length
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                        COMMENT
                                                                                                                                                                                     During sequence seembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation amotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with conly a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORNDEP; Information on the WORNDEP; database can be found at the sanger ac.uk/Projects/C_elegans/wormpep This sequence chromosome 10, constructed by the Sanger Centre Chromosome 10 http://www.sanger.ac.uk/HGPP/Chromosome Chromosome 10 http://www.sanger.ac.uk/HGPP/Chromosome 20 http://www.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.sanger.ac.uk/HGP/Chr10
RP11-67C2 is from the library RPC1-11.1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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1-16F14, WORKING DRAFT SEQUENCE, 30 unordered
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Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B.,
Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo, sapiens, clone RP11-16P14
        Trust Sanger Institute, Hinxton,
Submitted (31-MAY-2002) Wellcome Trust Sanger Institute, Hinxton Cambridgeshire, CBIO 18A, UK. B-mail enquiries in the CBIO 18A, UK. B-mail enquiries is the Munguery@aanger.ac.uk Clone requests: clonerequestesanger.ac.uk On Jun 21, 2002 this sequence version replaced gi:21213582. Draft Sequence Produced by Genome Therapeutics Corp, 100 Beaver Street, Waltham, MA 02453, USA
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100.0%; Pred. No. 0.00035
ive 0; Mismatches (
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db_xref="taxon:9606"
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/clone_lib="RPCI-11.1"
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Homo sapiens (human)
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VECTOR: pBACe3.6.
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AC010862 194453 bp DNA linear HTG 30-AUG-2001
Homo sapiens chromosome 06 clone RP11-326D18, WORKING DRAFT
SEQUENCE, 25 unordered pieces.
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Direct Submission
Submitted (25-SEP-1999) Genome Therapeutics Corporation, 100 Beaver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (base 1 to 194453)
Smith, D.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing vector: N/A
Chemistry: Dye-terminator Big Dye; 100% of reads
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On Sep 1, 2000 this sequence version replaced gi:8247773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 94.1%; Score 48; DB 2; Length 160654; Best Local Similarity 100.0%; Pred. No. 0.00037; Matches 48; Conservative 0; Mismatches 0; Indels 0
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------ Project Information
Center project name: hg024
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Web site: http://www.genomecorp.com/
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AC010862.7 GI:9957987
HOMO SADIENS (human)
HOMO SADIENS (human)
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55414. 675594 fragment"
/note="assembly_fragment"
63695. 73843 /note="assembly_fragment"
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83766. .9522
/note="assembly_fragment"
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145798. .160654
/note="assembly_fragment"
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36727. .42109
/note="assembly_fragment"
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/note="assembly_fragment"
48440. .55333
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2 (bases 1 to 194453)
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120220: contig of 11717 bp in length
120320: gap of 100 bp
132958: contig of 12638 bp in length
134569: contig of 12639 bp in length
145697: contig of 12639 bp in length
145797: gap of 100 bp
160654: contig of 14857 bp in length
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/db xref="taxon.9606"
/clone="RP11-16P14"
/clone lib="RPCI-11 Human Male BAC"
1.151
/note="assembly_fragment
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//note="assembly_fragment"
12960. .15671
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15772. .18082
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/note="assembly_fragment"
25642. . . 28323
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/note="assembly_fragment"
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/note="assembly_fragment"
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/note="assembly_fragment"
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/note="assembly_fragment"
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'note="assembly_fragment'
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note="assembly_fragment"
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1. .160654
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252. .1760
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/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
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Diagnosis of diseases associated with signal transduction
Patent: WO 0200926-A 19 03-UAN-2002;
Epigenomics AG (DE)
Location/Qualifiers
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Pred. No. 0.33;
0; Mismatches 6;
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                         94.1%; Score 48; DB 100.0%; Pred. No. 0.0 iive 0; Mismatches
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Sequence 20 from Patent WO0200926.
AX344173
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Sequence 19 from Patent W00200926.
AX344172
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1 Similarity 87.5%;
42; Conservative 0
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Best Local Similarity 87.5%;
Matches 42; Conservative
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Assembly program: Phrap, version 990315
Consensus quality: 162991 bases at least Q40
Consensus quality: 176452 bases at least Q30
Consensus quality: 179870 bases at least Q20
Insert size: 192053; sum-of-contigs
Quality coverage: 4.2x in Q20 bases; sum-of-contigs
                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 25 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10895: Gortig of 1274 pin length 10995: gap of unknown length 12283: gap of unknown length 12283: gap of unknown length 13602: contig of 1188 bp in length 13702: gap of unknown length 13702: gap of unknown length 16055: gap of unknown length 16253: gap of unknown length 18397: contig of 2242 bp in length 18397: contig of 5274 bp in length 1837: gap of unknown length 24368: gap of unknown length 24468: gap of unknown length 3049: gap of unknown length 3049: contig of 5581 bp in length 3049: gap of unknown length 30591: contig of 6812 bp in length 43997: contig of 6812 bp in length 43997: contig of 6816 bp in length 43997: contig of unknown length 43097: gap of unknown length
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contig of 5843 bp in length
gap of unknown length
contig of 6947 bp in length
gap of unknown length
contig of 8454 bp in length
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85520: gap of unknown length
101885: contig of 16365 bp in length
101985: gap of unknown length
124008: contig of 22023 bp in length
124108: gap of unknown length
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                                                                                                                                                                                                                                                                                                                                                              1117: contig of 1117 bp in length
1217: gap of unknown length
2365: contig of 1148 bp in length
2465: gap of unknown length
3576: contig of 1111 bp in length
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contig of 1167 b
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PAT 06-FEB-2002

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Length 13249

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Human DNA sequence from clone RP11-394123 on chromosome 10, ALS90439 ALS90430.12 GI:153848?
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 192044)
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/note="chemically treated genomic DNA (Homo sapiens)"
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Direct Submission
Submitted (23-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
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/note="chemically treated genomic DNA (Homo sapiens)"
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Diagnosis of diseases associated with cell signalling
Patent: WO 0202807-A 21 10-JAN-2002;
Epigenomics AG (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Olek,A., Piepenbrock,C. and Berlin,K. Diagnosis of diseases associated with cell signalling Petent: WO 0202807-A 22 10-JAN-2002; Epigenomics AG (DE)
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Sequence 22 from Patent WO0202807.
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Homo sapiens
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                                                                                                                                                                                                                                                                                         /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/noTe="chemically treated genomic DNA (Homo sapiens)"
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
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Diagnosis of diseases associated with the immune system
Patent: WO 0200928-A 89 03-JAN-2002;
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Diagnosis of diseases associated with the immune system
Patent: WO 0200928-A 90 03-JAN-2002;
Epigenomics AG (DE)
Location/Qualifiers
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                                              linear
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Pred. No. 0.33;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          75.3%; Score 38.4; DB 87.5%; Pred. No. 0.33;
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                                           AX345018 13249 bp
Sequence 89 from Patent W00200928.
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Sequence 21 from Patent W00202807.
AX348563
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Sequence 90 from Patent W00200928.
AX345019
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1 Similarity 87.5%;
42; Conservative
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          RESULT 6
AX345018
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COMMENT

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Summary Statistics of Sases at least Q40 Consensus quality: 114565 bases at least Q30 Consensus quality: 124565 bases at least Q30 Consensus quality: 124565 bases at least Q30 Estimated insert size: 127829; sum-of-contigs estimation Quality coverage: 4.26 in Q20 bases; pulse field gel estimation Quality coverage: 4.26 in Q20 bases; pulse field gel estimation.

**OUTE: This is a "working draft' sequence It currently consists of 16 contigs. Gaps between the contigs.

**A TEP TROUGHT OF CONTIGS. Gaps between the sizes of the gaps between them are based on estimates that have provided by the submittor.

**This sequence will be replaced.

**Pins sequence will be replaced.

**Pins sequence will be preserved.

*
Score 33.6; DB 2; Length 128529; Pred. No. 3.8;
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/clone="CTD-2235A13"
/clone_lib="CalTech human BAC library D"
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Location/Qualifiers
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                                                                                                                                                                                        Web site: http://www.jgi.doe.gov
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/organism="Homo sapiens'
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/db xref="taxon:9606"
                                                                                                                                                                                                                                                                                    Center Project Name: 717802
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81.2%;
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Best Local Similarity 81.2:
Matches 39; Conservative
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      requencie: cloud this sequence version replaced gi:14268248.

On Aug 31, 2001 this sequence version replaced gi:14268248.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the overlapping clone name. Note that the corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) as compressions and repeats; all regions were covered by as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SMISSPROT; T::, TREMBL; WORNERP; Information on the WORNERP HITH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.chori.org/bacpac/home.htm
VECTOR: place3.6
IMPORTANT: This sequence is not the entire insert of clone
SECTIONS only once, except for a short overlap.
The true right end of clone RPI1-394123 is at 192044 in this sequence. The true left end of clone RPI1-394123 is at 182044 in this sequence. The true left end of clone RPI1-65789 is at 18254 in this sequence. The true right end of clone RPI1-3945 is at 18204 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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CTD-2235A13, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at Mapping Group. Further information can be found at RRD1-394123 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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0; Mismatches
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/clone_lib="RPC1-11.2"
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Unpublished
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HTG; HTGS_PHASE2; HTGS_DRAFT.
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SEQUENCE, 16 ordered pieces
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DOE Joint Genome Institute.
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KEYWORDS

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REFERENCE AUTHORS

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ACCESSION VERSION KEYWORDS

ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

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JOURNAL REFERENCE

TITLE JOURNAL AUTHORS

COMMENT

FEATURES

ORIGIN

TITLE JOURNAL

AUTHORS

REFERENCE

REFERENCE AUTHORS TITLE JOURNAL

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BS000239 209016 bp DNA linear PRI 07-0CT-2003 Pan troglodytes chromosome 22 clone:PTB-153E07, map 22, complete
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*Chinase National Human Genome Center at Shanghai, Shanghai, China;
*GBF, Dept. of Genome Analysis, Braunschweig, Germany; *Institute
of Molecular Biotechnology, Jena, Germany; *KRIBB Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (16-MAY-2003) Shih-Feng Tsai, National Health Research Institutes (NHRI), Division of Molecular and Genomic Medicine; 128, Yen-Chiu-Yuan Road, Sec 2, Taipei 115, Taiwan (E-mail:petsai@nhi.org.tw, URL:http://www.nhri.org.tw/, Tel:886-2-28246)139, Fax:886-2-28200552)
                                                                                                                                                                                                                                                         Direct Submission
Submitted (16-AUG-2001) Production Sequencing Facility, DOE Joint
Submitted (16-AUG-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (Dases 1 to 164217)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (01-FBB-2002) DOB Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Feb 1, 2002 this sequence version replaced gi:15193398.
Draft Sequence Produced by DOB Joint Genome Institute
                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 164217)
DOB Joint Genome Institute and Stanford Human Genome Center.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Pan.
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DNA sequence of chimpanzee chromosome 22 and its evolutionary
implications
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www-shgc.stanford.dom
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.1.
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2 (bases I to 209016)
15ai,S., Liu,T., Wu,K., Liao,T. and Hsiao,K.
Direct Submission
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/chromosome="5"
/clone="RP11-263G2"
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Unpublished
2 (bases 1 to 164217)
DOB Joint Genome Institute.
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BS000239.1 GI:37537506
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Homo sapiens (human)
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                                                                                                                                                                                                                 PRI 28-JUN-2003
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Submitted (28-0704-2003) DOB Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Jun 28, 2003 this sequence version replaced gi:14993661.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                              Eukarrotta.

Eukarrotta, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

I (Dases I to 157325)

DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission
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Submitted (26-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
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Direct Submitted end Stanford Human Genome Center.
Direct Submitted (21-JUL-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walhut Creek, CA 94598, USA
5 (bases 1 to 157325)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                             ACO08810 157325 bp DNA linear PRI 28-JUN
Homo sapiens chromosome 5 clone CTD-2096123, complete sequence
ACO08810
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Quality: Phrap Quality >=40 99.7% of Sequence;
Estimated Total Number of Errors is 0.3.
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/db_xref="taxon:9606"
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clone="CTD-2096123"
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DOE Joint Genome Institute.
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DEFINITION ACCESSION VERSION

KEYWORDS

RESULT 13 AC093264 LOCUS

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Blakey, S. Canding and Trust Sanger Institute, Hinxton, Submission
Submission
Submission
Cambridgeshire, CB10 15A, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Apr 7, 2002 this sequence version replaced gi:141359.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SANISSPROT; Tr:, TREMBL; WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                           ROD 29-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                     AL365334 173053 bp DNA linear ROD 29-JUN-2002
Mouse DNA sequence from clone RP23-392F1 on chromosome 1, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musi
1 (bases 1 to 173053)
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                                                                                                                                                                                                                                                123272 AAATAAATAAATTGGGCTTAAAATTAAAACTTTTGTGCTTGCAAGGACAT 123222
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80.9%; Pred. No. 6.6;
tive 0; Mismatches 9;
                                                                                    ch 65.5%; Score 33.4; DB 9; 1 Similarity 78.4%; Pred. No. 3.8; 40; Conservative 0; Mismatches 11;
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Center code: UK-MRC
Web site: http://mrcseg.har.mrc.ac.uk
'note="low quality region"
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/db_xref="taxon:10090"
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/clone="RP23-392F1"
/clone_lib="RPCI-23"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          For lux...-
VECTOR: pBACe3.6
Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL365334.13 GI:20068419
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Best Local Similarity
Matches 38; Conserv
                                                                                                                   Best Local Similarity
                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                             RESULT 15
AL365334/c
                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
                                                                                                                                                  Matches
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Source information:
The PTB1 chimpanzee BAC library was prepared from DNA isolated from
cultured cells established from the blood of a single male
                                                                                                                                                  ------ Genome Center
Center: National Yang Ming University Genome Research Center Center
                                                                                                                                                                                                                                                                  This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This entry has been annotated with sequence estimates computed by the Phrap assembly program. All manually edited base have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in
                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: pUC18; 100% of reads
Sequencing vector: pUC18; 100% of reads
Chemistry: Dye-terminator Big Dye and BT; 100% of reads Assembly
program: Phrap; version 0.990319
Consensus quality: 207,750 bases at least Q40
Consensus quality: 207,996 bases at least Q30
Consensus quality: 208,014 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="gap containing unresolved di-nucleotide repeats,
*Max-Planck-Institute for Molecular Genetics, Berlin, Germany, *National Institute of Genetics, Mishima, Japan; *National Yang Ming University Genome Research Center, Taipei, *National Yang Ming University Genome Research Center, Taipei,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   an attempt was made to resolve all sequencing problems, such compressions and repeats; all regions were covered by at one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neighboring clones: PTB-152N20(left) and RP43-055A16(right) Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clones may be obtained from Asao Fujiyama and co-workers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.
                                                                                                                      *RIKEN Genomic Sciences Center, Yokohama, Japan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="PTB-153E07"
/clone_lib="PTB1 chimpanzee BAC"
16459. .16463
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46232. .46235
/note="low quality region"
46277. .46280
/note="low quality region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="low quality region"
128691
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/note="low quality region"
43909. .44908
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                                                                                                                                                                                                                                          Web site: http://genome.ym.edu.tw/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic_DNA"
/db_xref="taxon:9598"
/chromosome="22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence Quality Assessment:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (http://www.gsc.riken.go.jp)
VECTOR: pKS145
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                                                                                                                                                                                                             code: XMGC
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Search completed: May 7, 2004, 14:30:58 Job time : 538.003 secs